

GerCore version 5.1.6  
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CM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 20:23:15 ; Search time 213 Seconds  
(without alignments)

Title: US-09-676-436-3 COPY 3264 3383

US-09-076-430-3\_COP1\_2404\_3383  
 120  
 Perfect score: 120  
 Sequence:  
 1 tcaatgcccatgaagccctg.....gctgcgaatttcaagatttag 120

scoring table: IDENTITY NIK

SCORING TABLE:	IDENTITY_NOC
Gapop	10.0
Gapext	1.3

Searched: 2185239 seqs, 1125999159 residues

Total number of hires satisfying chosen parameters: 2165242

Minimum DB seq length: 8

minimum DB seq	length: 8
maximum DB seq	length: 50

Post-processing: Minimum March 03

Post-processing:	Minimum	Match	Score
	Whitlock	Match	100%

Maximum Match 100%  
Listing first 200 summaries

```

Database :
1: SIDS1/acgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: SIDS1/acgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: SIDS1/acgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: SIDS1/acgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: SIDS1/acgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: SIDS1/acgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: SIDS1/acgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: SIDS1/acgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: SIDS1/acgdata/geneseq/geneseq-emb1/NA1988.DAT.*
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19: SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
21: SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001.DAT.*
22: SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
23: SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

```

ppred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	20.4	17.9	45	18	AA031362	Biotinylated inter-
C 2	20	16.9	20	24	AA031362	Human CD45 anti-
C 3	20	16.7	20	24	AA037703	Human MEK4 anti-
C 4	19.2	16.0	48	20	AA076673	Human SV4 library
C 5	19	15.8	47	21	AA068493	Human map-related
C 6	18.4	15.3	40	16	AA091033	HRV-6 associated m
C 7	18.2	15.2	47	15	AA078509	Neomycin resistant m
C 8	18.2	15.2	47	21	AA068328	Human map-related
C 9	17.8	14.8	38	20	AA005511	Synthetic Pn3 gene

C 83	15.8	13.2	45	20	AA52480	Probe used to iso	156	15.4	12.8	42	21	AA53532	Secreted alkaline
C 84	15.8	13.2	45	22	AA52638	Human PRO polyepit	157	15.4	12.8	42	21	AA528743	Sense primer for C
C 85	15.8	13.2	45	24	ABX2585	Human PRO346 hypr1	158	15.4	12.8	42	21	AAA13695	Human SEAP gene PC
C 86	15.8	13.2	47	21	AA267091	Human map-related	159	15.4	12.8	42	21	AAA13776	Human SEAP gene PC
C 87	15.8	13.2	47	21	AA267970	Human map-related	160	15.4	12.8	42	21	AA290101	PCR primer used to
C 88	15.8	13.2	47	21	AA268911	Human map-related	161	15.4	12.8	42	21	AA260494	PCR primer used to
C 89	15.8	13.2	47	22	AA503322	Bacterial 235/55 R	162	15.4	12.8	42	21	AA258849	Human SEAP gene am
C 90	15.8	13.2	50	22	AA525966	Rice genomic fragm	163	15.4	12.8	42	21	AA235454	SEAP C-terminal re
C 91	15.8	13.2	27	18	AA529777	Plasmid pET-E2.123	164	15.4	12.8	42	21	AA235473	Human SEAP C-termi
C 92	15.8	13.2	27	18	AA529777	Primer E21 for BP	165	15.4	12.8	42	22	AA514790	Sense strand C-ter
C 93	15.8	13.2	27	18	AA529777	Tat-E2 conjugate P	166	15.4	12.8	42	22	AA514790	Human SEAP C-ter
C 94	15.8	13.2	27	19	AA529777	Tat-E2 conjugate P	167	15.4	12.8	42	22	AA514790	Human SEAP gene am
C 95	15.8	13.2	31	17	AA529777	Bovine papillomavi	168	15.4	12.8	42	22	AAH47773	PCR primer for C-t
C 96	15.8	13.2	31	17	AA529777	Murine 103 gene fo	169	15.4	12.8	42	22	AAH47773	PCR primer used to
C 97	15.8	13.2	31	21	AA51910	Forward primer for	170	15.4	12.8	42	22	AAH47773	PCR primer used to
C 98	15.8	13.2	31	21	AA51910	Mouse 103 gene for	171	15.4	12.8	42	22	AAH47773	PCR primer 3 used
C 99	15.8	13.2	31	22	AA503380	5' primer, to ampl	172	15.4	12.8	42	22	AAH47773	Human B-cell trans
C 100	15.8	13.2	31	22	AA503380	Murine TH2-enrich	173	15.4	12.8	42	22	AAH47773	Human SEAP gene se
C 101	15.8	13.2	31	22	AA503380	Mouse 103 gene pro	174	15.4	12.8	42	22	AAH47773	Human SEAP CDNA sp
C 102	15.8	13.2	31	22	AA503380	5' oligonucleotide	175	15.4	12.8	42	22	AAH47773	Human SEAP PCR pri
C 103	15.8	13.2	31	22	AA503380	Primer Bstqk-G2 fo	176	15.4	12.8	42	22	AAH47773	Human SEAP PCR pri
C 104	15.8	13.2	31	22	AA503380	Oligonucleotide en	177	15.4	12.8	42	22	AAH47773	Human SEAP PCR pri
C 105	15.8	13.2	31	22	AA503380	Human peroxidase 1	178	15.4	12.8	42	22	AAH47773	Human SEAP gene am
C 106	15.8	13.2	31	22	AA503380	Probe 669, hybrid	179	15.4	12.8	42	22	AAH47773	Human SEAP gene am
C 107	15.8	13.2	31	22	AA503380	PCR primer SNS-Up	180	15.4	12.8	42	22	AAH47773	Human SEAP gene am
C 108	15.8	13.2	31	22	AA503380	Human map-related	181	15.4	12.8	42	22	AAH47773	PCR primer 13 used
C 109	15.8	13.2	31	22	AA503380	Human map-related	182	15.4	12.8	42	22	AAH47773	Sense strand C-ter
C 110	15.8	13.2	31	22	AA503380	PCR primer used to	183	15.4	12.8	42	22	AAH47773	Human SEAP gene se
C 111	15.8	13.2	31	22	AA503380	PCR sense primer f	184	15.4	12.8	42	22	AAH47773	Human SEAP gene se
C 112	15.8	13.2	31	22	AA503380	Nucleotide sequenc	185	15.4	12.8	42	22	AAH47773	Human SEAP gene se
C 113	15.8	13.2	31	22	AA503380	Plasmid pVLMB DNA	186	15.4	12.8	42	22	AAH47773	Sense PCR primer u
C 114	15.8	13.2	31	22	AA503380	Oligonucleotide #5	187	15.4	12.8	42	22	AAH47773	Synthetic fn3 gene
C 115	15.8	13.2	31	22	AA503380	Nucleotide sequenc	188	15.4	12.8	42	22	AAH47773	Fibronectin 3 codi
C 116	15.8	13.2	31	22	AA503380	Human PRO230 hybr	189	15.4	12.8	42	22	AAH47773	Granulocyte-colony
C 117	15.8	13.2	31	22	AA503380	Probe used to isol	190	15.4	12.8	42	22	AAH47773	Nitrocellulose-bin
C 118	15.8	13.2	31	22	AA503380	EGF-like/FGF-8 hom	191	15.4	12.8	42	22	AAH47773	Two member family
C 119	15.8	13.2	31	22	AA503380	Probe used for PRO	192	15.4	12.8	42	22	AAH47773	Synthetic plasmid
C 120	15.8	13.2	31	22	AA503380	Probe for PRO230 n	193	15.4	12.8	42	22	AAH47773	2'NH2 RNA ligand t
C 121	15.8	13.2	31	22	AA503380	Human SNP oligonuc	194	15.4	12.8	42	22	AAH47773	2'NH2 RNA ligand t
C 122	15.8	13.2	31	22	AA503380	Human PRO230 hybr	195	15.4	12.8	42	22	AAH47773	PCR primer used in
C 123	15.8	13.2	31	22	AA503380	PRO230 probe #1	196	15.4	12.8	42	22	AAH47773	Tag sequence of a
C 124	15.8	13.2	31	22	AA503380	Human PRO polyepit	197	15.4	12.8	42	22	AAH47773	T.n1 acyl-CoA del
C 125	15.8	13.2	31	22	AA503380	Neuropeptide FF re	198	15.4	12.8	42	22	AAH47773	Sequence of CDC23
C 126	15.8	13.2	31	22	AA503380	PCR primer for cDN	199	15.4	12.8	42	22	AAH47773	Cmr fragment PCR p
C 127	15.8	13.2	31	22	AA503380	E. coli tyrA PCR p	200	15.4	12.8	42	22	AAH47773	
C 128	15.8	13.2	31	22	AA503380	Prn(S)psbD(S) reg							
C 129	15.8	13.2	31	22	AA503380	Human endoenzyme C							
C 130	15.8	13.2	31	22	AA503380	Sequence binding t							
C 131	15.8	13.2	31	22	AA503380	NGFR5par, targette							
C 132	15.8	13.2	31	22	AA503380	P. fluorescens asp							
C 133	15.8	13.2	31	22	AA503380	Saccharomycos cere							
C 134	15.8	13.2	31	22	AA503380	Yeast ELO2 PCR pri							
C 135	15.8	13.2	31	22	AA503380	PCR primer used to							
C 136	15.8	13.2	31	22	AA503380	M31X22 vector con							
C 137	15.8	13.2	31	22	AA503380	Primer 016 for con							
C 138	15.8	13.2	31	22	AA503380	First reverse PCR							
C 139	15.8	13.2	31	22	AA503380	M31X11 translatio							
C 140	15.8	13.2	31	22	AA503380	PCR primer 306 use							
C 141	15.8	13.2	31	22	AA503380	Maize polymorphic							
C 142	15.8	13.2	31	22	AA503380	Eukaryotic initiat							
C 143	15.8	13.2	31	22	AA503380	Human B-cell trans							
C 144	15.8	13.2	31	22	AA503380	Human B-cell trans							
C 145	15.8	13.2	31	22	AA503380	Sense PCR primer u							
C 146	15.8	13.2	31	22	AA503380	Human SEAP gene PC							
C 147	15.8	13.2	31	22	AA503380	Primer for amplif							
C 148	15.8	13.2	31	22	AA503380	SEAP reporter plas							
C 149	15.8	13.2	31	22	AA503380	SEAP reporter plas							
C 150	15.8	13.2	31	22	AA503380	SEAP reporter plas							
C 151	15.8	13.2	31	22	AA503380	SEAP reporter plas							
C 152	15.8	13.2	31	22	AA503380	Sense strand C-ter							
C 153	15.8	13.2	31	22	AA503380	Human secreted alk							
C 154	15.8	13.2	31	22	AA503380	Human secreted alk							
C 155	15.8	13.2	31	22	AA503380	Human secreted alk							

## ALIGNMENTS

RESULT 1  
AAV03162/C  
ID AAV03162 standard; DNA: 45 BP.  
XX  
AC AAV03162:  
XX  
DT 08-APR-1998 (first entry)  
XX  
DE Biotinylated interleukin-8 consensus ligand sequence 1 DNA.  
XX  
KW Bacteriophage peptide library: peptide epitope; therapeutic target:  
XX variegated compound library; ss.  
OS Synthetic.  
XX  
PN W09735194-A2.  
XX  
PD 25-SEP-1997.  
XX  
PF 21-MAR-1997; 97WO-US04176.  
XX  
PR 21-MAR-1996; 96US-0622338.



AAD37203/C  
 ID AAD37203 standard; DNA: 20 BP.  
 AC AAD37203:  
 XX  
 XX 21-AUG-2002 (first entry)  
 XX Human MEKK4 antisense oligonucleotide, ISIS #123138.  
 DE Human: MEKK4 modulation: mitogen-activated protein kinase kinase 4; MTX1;  
 KW MAP3K4; MAP three kinase 1; MAP/ERK kinase 4; MAPKKK4; cytosolic;  
 KW prolylase; immunological; hyperproliferative disorder; cancer; therapy;  
 KW antisense; inflammatory; phosphorothioate backbone; ss.  
 XX Homo sapiens.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag- a  
 FT /mod\_base- OTHER  
 FT /note- "Phosphorothioate backbone"  
 FT modified\_base 1..5  
 FT /\*tag- b  
 FT /mod\_base- OTHER  
 FT /note- "2'-methoxyethyl nucleotides"  
 FT modified\_base 16..20  
 FT /\*tag- c  
 FT /mod\_base- OTHER  
 FT /note- "2'-methoxyethyl nucleotides"  
 FT modified\_base 3  
 FT /\*tag- d  
 FT /mod\_base- m5c  
 FT modified\_base 6  
 FT /\*tag- e  
 FT /mod\_base- m5c  
 FT modified\_base 15  
 FT /\*tag- f  
 FT /mod\_base- m5c  
 FT modified\_base 16  
 FT /\*tag- g  
 FT /mod\_base- m5c  
 FT modified\_base 20  
 FT /\*tag- h  
 FT /mod\_base- m5c  
 XX WO200227033-A1.  
 XX 04-APR-2002.  
 XX 28-SEP-2001: 2001WO-US30549.  
 XX 29-SEP-2000: 2000US-0676436.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Ward DT, Gaarde WA, Monia BP, Wyatt JR;  
 XX WPI: 12002-416486/44.  
 XX New antisense compound targeted to nucleic acid encoding  
 PT mitogen-activated protein kinase 4, useful for treating immunologic  
 PT disorder, inflammatory disorder or cancer  
 XX  
 PS Claim 3: Page 93: 133pp: English.  
 CC The present invention relates to antisense compounds, compositions and  
 CC methods for modulating the expression of MEKK4 (also referred to as mitogen-  
 CC activated protein kinase kinase 4; MAP3K4; MAP three kinase 1; MAP/ERK  
 CC kinase kinase 4; MAPKKK4; MTX1). The antisense oligos are useful for  
 CC inhibiting the expression of MEKK4 in cells or tissues. They are also  
 CC useful for treating an animal having a disease or condition associated  
 CC with MEKK4 such as immunological, inflammatory, hyperproliferative

CC disorder or cancer. Sequences of the invention are also useful for  
 CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.  
 CC They are also useful in antisense therapy. The present sequence is an  
 CC antisense oligonucleotide targeted to human MEKK4 DNA. This sequence  
 CC is used in the exemplification of the invention.  
 XX  
 SQ Sequence 20 BP: 7 A: 5 C: 5 G: 3 T: 0 other:  
 Query Match 16.7% Score 20: DB 24: Length 20;  
 Best Local Similarity 100.0% Pred No. 1.1e+03;  
 Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 QY 87 GATTGGCTTCATAGCTGCT 106  
 DB 20 GATTGGCTTCATAGCTGCT 1  
 RESULT 4  
 AAX76673  
 ID AAX76673 standard; DNA: 48 BP.  
 XX  
 AC AAX76673:  
 XX  
 XX 11-AUG-1999 (first entry)  
 XX Human sfv library construction PCR primer SEQ ID NO:85.  
 DE Human: sfv library: single chain monoclonal antibody fusion reagent;  
 KW transcription regulation; screening; diagnosis; HIV; Hepatitis A;  
 KW Hepatitis B respiratory syncytial virus; Junin virus; cytomegalovirus;  
 KW Herpes simplex virus; rubella; Varicella-Zoster virus; hantavirus;  
 KW Epstein-Barr virus; measles; dengue; Ebola inter alia; cancer;  
 KW gene therapy; PCR primer; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO9928502-A1.  
 PN 10-JUN-1999.  
 PD 28-NOV-1997: 97WO-US21407.  
 XX 28-NOV-1997: 97WO-US21407.  
 PR (INVI-) INVITROGEN CORP.  
 PA Hoeftler JP, Russell M;  
 PI WPI: 1999-371138/31.  
 DR Antibodies from libraries useful in treating viral infections and  
 XX cancer  
 PS Claim 23: Page 108: 132pp: English.  
 CC The present invention describes methods of screening a DNA construct  
 CC library for a single chain monoclonal antibody fusion reagent capable  
 CC of binding a transcriptional associated biomolecule in vivo. The  
 CC antibodies are useful in treating Hepatitis A and B respiratory  
 CC syncytial virus, HIV, Junin virus, Herpes simplex I and II, rubella,  
 CC cytomegalovirus, Varicella-Zoster virus, Epstein-Barr virus, measles,  
 CC hantavirus, dengue, Ebola inter alia and cancer. Expression vectors  
 CC that encode the fusion antibodies may be used in gene therapy. The  
 CC methods can be used to create and isolate the fusion antibodies. The  
 CC monoclonal antibody fusion reagent can be used to regulate  
 CC transcription in vivo. AAX76591 to AAX76674 represent specifically  
 CC claimed PCR primers used in the construction of a human sfv library.  
 XX Sequence 48 BP: 10 A: 14 C: 12 G: 12 T: 0 other:  
 Query Match 16.0% Score 19.2: DB 20: Length 48;  
 Best Local Similarity 62.5% Pred. No. 2.9e+03;





Gene transfer: Human GRP78; glucose-regulated protein; BiP;  
immunoglobulin heavy chain binding protein; IRES;  
internal ribosome entry site; polycistronic retroviral vector;  
neomycin phosphotransferase; neomycin resistance; ss.

Synthetic.  
WO9424870-A.  
10-NOV-1994.  
17-JAN-1994: 94WO-US00650.  
20-JAN-1993: 93US-0006478.  
(BIOT) BIOTRANSPLANT INC.  
(GEHO) GEN HOSPITAL CORP.  
Banerjee PT, Seed B, Le Guern CA;  
WPI; 1994-357763/44.  
Retroviral vectors - express multiple polypeptide subunits of  
eukaryotic protein and useful for mediating gene transfer  
Example 1: Page 35; 63pp: English.  
A neomycin resistance gene-contg. DNA fragment was generated by PCR  
using primer Exneo (AA078509) which contains nucleotides 149-177 of  
the neomycin phosphotransferase gene and sites for EcoRI and XhoI.  
CC and primer BglII-linked 3' neomycin (AA078510) which contains the  
reverse complement to the neomycin resistance gene nucleotides  
922-945 and a BglII site. The PCR fragment was used in the  
construction of a polycistronic vector pBMS for expression of  
neomycin phosphotransferase; the vector also contained a BiP  
IRES-containing DNA fragment.

Query Match 15.24; Score 18.2; DB 15; Length 47;  
Best Local Similarity 66.74; Pred. No. 6.5e+03;  
Matches 26; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 53 GGATTCAGCGGTCCTCGAATGATCGATTG 91  
DB 3 GAATTCAGCGGTCCTCGAATGATCGATTG 41  
RESULT 8  
AAZ68328  
ID AAZ68328 standard; DNA: 47 BP.  
AC AAZ68328;  
DT 10-SEP-2001 (first entry)  
DE Human map-related biallelic marker SEQ ID NO:2675.  
XX Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation;  
KW diagnosis; single nucleotide polymorphism; SNP; ds.  
XX Homo sapiens.  
XX Location/Qualifiers  
FH Key  
FT variation  
FT replace(24.G)  
FT /tag=a  
FT /standard\_name="single nucleotide polymorphism"  
PN WO9954500-A2.  
XX 28-OCT-1999.

21-APR-1999; 99WO-IB00822.  
21-APR-1998; 98US-0082614.  
23-NOV-1998; 98US-0109732.  
(GEST) GENSET.  
Cohen D, Blumenfeld M, Chumakov I;  
WPI; 2000-013267/01.  
Novel biallelic markers used to construct a high density disequilibrium  
map of the human genome -  
Claim 3; Page 801; 2745pp: English.  
AAZ65654 to AAZ69578 represent human biallelic markers from the present  
invention, which contain a polymorphic base at position 24 of their  
nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
primers for the biallelic markers. The biallelic markers of the  
invention have a variety of uses: they can be used for high density  
mapping of the human genome, and in complex association studies and  
haplotyping studies which are useful in determining the genetic basis  
for disease states. Compositions and methods of the invention can also  
be useful for the identification of the targets for the development of  
pharmaceutical agents and diagnostic methods, as well as the  
characterisation of the differential efficacious responses to and side  
effects from pharmaceutical agents acting on a disease as well as other  
treatment.  
N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297  
and 3367, are not actually given a sequence in the Sequence Listing  
from the present invention.  
XX Sequence 47 BP; 9 A; 15 C; 7 G; 16 T; 0 other;  
Query Match 15.24; Score 18.2; DB 21; Length 47;  
Best Local Similarity 74.24; Pred. No. 6.5e+03;  
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 47 CCACGGGATTCAGCGGTCCTCGGTCCTG 77  
DB 12 CCAATTGATTCAGCTAGTTCAGCTCCCTG 42  
RESULT 9  
AAZ05511  
ID AAZ05511 standard; DNA: 38 BP.  
AC AAZ05511;  
DT 14-APR-1999 (first entry)  
DE Synthetic Fn3 gene constructing oligo FN5R'.  
KW Fibronectin type III; Fn3; monobody; beta-strand domain; loop region;  
KW specific binding partner; SBP; catalysis; LRS; ss.  
XX Synthetic.  
XX Homo sapiens.  
PN WO9856915-A2.  
XX 17-DEC-1998.  
XX 12-JUN-1998; 98WO-US12099.  
PR 12-JUN-1997; 97US-0049410.  
XX (RESE) RESEARCH CORP TECHNOLOGIES INC.  
XX Koide S.  
XX





RESULT 14  
 AAT88162/C  
 ID AAT88162 standard; DNA: 45 BP.  
 XX  
 AC AAT88162;  
 XX  
 DT 11-MAY-1998 (first entry)  
 XX  
 DE PCR primer JM20.  
 XX  
 KW Autotransporter; diagnostic; therapy; Gram-negative bacteria;  
 KM surface presented polypeptide; fusion protein; PCR primer: ss.  
 XX  
 OS Synthetic.  
 XX  
 PM WO9735022-A1.  
 XX  
 PD 25-SEP-1997.  
 XX  
 PF 15-MAR-1996; 96WO-EP01130.  
 XX  
 PR 15-MAR-1996; 96WO-EP01130.  
 XX  
 PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PI Jose J. Maurer J. Meyer TF;  
 XX  
 DR WPI: 1997-480227/44.  
 XX  
 PT Presentation of peptide(s) on surface of Gram-negative bacteria  
 XX via transformation with vector encoding signal peptide, presented  
 XX peptide and transporter domain of auto-transporter, producing  
 XX peptide libraries for epitope mapping  
 XX  
 PS Example 3; Fig 6; 84pp; German.  
 XX  
 CC PCR primers AAT88158-788162 are used in the construction of surface  
 CC exposed fusion proteins containing a bacterial autotransporter membrane  
 CC integration region with the antigenic determinant of a passenger  
 CC protein. Such proteins are used in a novel method which allows the  
 CC presentation of peptides on the surface of Gram-negative bacteria.  
 CC The method can be used to produce a variegated population of  
 CC surface-presented polypeptides, so that bacteria expressing polypeptides  
 CC with particular properties can be identified and simultaneously selected,  
 CC e.g. for epitope mapping or selection of ligands with the highest affinity  
 CC affinity for antibodies, major histocompatibility complex (MHC) molecules  
 CC or other components of the immune system. Selected polypeptides can be  
 CC used diagnostically, e.g. to screen sera or antibody banks, and  
 CC polypeptide expressing cells may be used as live vaccines. They may be  
 CC used therapeutically, e.g. when the polypeptide is an antibody to remove  
 CC or concentrate pollutants, inactivate toxins, prepare and process food,  
 CC prepare washing compositions and label cells. Selected bacteria can be  
 CC stored, reproduced and replicated on a large scale as individual clones.  
 XX  
 SQ Sequence 45 BP: 12 A: 6 C: 11 G: 16 T: 0 other:  
 Query Match 14.7% Score 17.6; DB 18; Length 45;  
 Best Local Similarity 65.0%; Pred. No. 1.1e+04;  
 Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
 Oy 28 ACACCTCATTCATCCCATCCAGGAGGATTCAGGGGTTC 67  
 Db 43 ACACCTCAAAAATTAATCTACTCGGAGTATTTCAAGGTACC 4  
 RESULT 15  
 ABK40757/C  
 ID ABK40757 standard; DNA: 47 BP.  
 XX  
 AC ABK40757;  
 XX  
 DT 21-MAY-2002 (first entry)  
 XX

XX Human obesity-associated chromosome 10 biallelic marker #5.  
 XX  
 KW Human: obesity associated-biallelic marker; chromosome 10; obesity; ds;  
 KM drug response; hyperuricaemia; digestive pathology; hypertension; cancer;  
 KW hepatic function disorder; cardiovascular disease; hyperlipidaemia;  
 KW insulin disorder; atherosclerotic disease; cardiac insufficiency.  
 XX  
 OS Homo sapiens.  
 XX  
 PM WO200206525-A2.  
 XX  
 PD 24-JAN-2002.  
 XX  
 PF 28-JUN-2001; 2001WO-1801477.  
 XX  
 PR 18-JUL-2000; 2000US-219704P.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Cohen D, Blumenfeld M, Chumakov I, Abderrahim R, Bihain B;  
 XX  
 DR WPI: 2002-155043/20.  
 XX  
 PT Set of novel map-related biallelic markers, preferably located on  
 XX obesity disorder-associated chromosomal regions on chromosomes 3, 10  
 XX and 19, useful, for e.g. detecting statistical correlations between  
 XX marker allele and a phenotype  
 XX  
 PS Claim 1; Page 193; 31pp; English.  
 XX  
 CC The invention relates to a set of novel map-related biallelic markers,  
 CC preferably located on obesity disorder-associated chromosomal regions on  
 CC chromosomes 3, 10 and 19. The markers are useful for genotyping or  
 CC estimating the frequency of an allele in a population, for detecting an  
 CC association between a genotype or haplotype and a phenotype, e.g. a  
 CC disease involving drug responses, obesity or disorders related to  
 CC obesity, such as hyperuricaemia, digestive pathology, hepatic function  
 CC disorders, cancer, cardiovascular disease, hypertension, hyperlipidaemia,  
 CC insulin disorders, atherosclerotic disease and cardiac insufficiency. The  
 CC markers are useful for detecting a statistical correlation between a  
 CC biallelic marker allele and a phenotype and/or between a biallelic marker  
 CC haplotype and a phenotype. The sequence presented is a biallelic marker  
 CC obesity-associated biallelic marker located on chromosome 10.  
 XX  
 SQ Sequence 47 BP: 9 A: 9 C: 11 G: 17 T: 1 other:  
 Query Match 14.7% Score 17.6; DB 24; Length 47;  
 Best Local Similarity 67.6%; Pred. No. 1.1e+04;  
 Matches 23; Conservative 1; Mismatches 10; Indels 0; Gaps 0;  
 Oy 22 TAACCCACACCTTATTCCTCCATCCAGGAGA 55  
 Db 35 TAACCCACACGACATCTTCAGCAGAGGCA 2  
 RESULT 16  
 ABL00311/C  
 ID ABL00311 standard; DNA: 50 BP.  
 XX  
 AC ABL00311;  
 XX  
 DT 05-MAR-2002 (first entry);  
 XX  
 DE Human silent noncoding SNP oligonucleotide SEQ ID NO:302.  
 XX  
 KW Human: single nucleotide polymorphism; SNP; polymorphism; cytosatic;  
 KM immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;  
 KM autoimmune disease; inflammation; cancer; nervous system disease;  
 KM infection; polymorphic protein; ds.  
 XX  
 OS Homo sapiens.  
 XX

PN WO200138586-A2.  
 XX 31-MAY-2001.  
 PD 22-NOV-2000; 2000MO-US32311.  
 PF 24-NOV-1999; 99US-0167383.  
 PR (CURA) CURAGEN CORP.  
 PA Shimklets RA, Leach M;  
 PI WPI: 2001-355949/37.  
 DR Isolated human nucleic acids comprising one or more single nucleotide  
 PT polymorphisms, useful for creating a subject suffering from a  
 PT pathology, e.g. autoimmune diseases, ascribed to the presence of a  
 PT sequence polymorphism.  
 XX Claim 1: Page 339; 674pp; English.  
 PS ABL00010 to ABL01104 represent human nucleic acid oligonucleotides  
 CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531  
 CC to ABB56903 represent human peptides encoded by some of the SNP  
 CC oligonucleotides. The sequences from the present invention can have  
 CC immunosuppressive, cytostatic, antitumorigenic, neuroprotective and  
 CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides  
 CC and antibodies from the present invention can be used for treating a  
 CC subject suffering from, at risk for, or suspected of, suffering from a  
 CC pathology ascribed to the presence of a sequence polymorphism. The  
 CC pathology may be autoimmune diseases, inflammation, cancer, diseases of  
 CC the nervous system, and infection by pathogenic microorganisms. The SNPs  
 CC are also useful for determining which forms of a characterised  
 CC polymorphism are present in individuals. The antibodies may be used in  
 CC the detection, quantitation and/or cellular or tissue localisation of a  
 CC polymorphic protein (e.g., for use in measuring levels of the  
 CC polymorphic protein within appropriate physiological samples).  
 XX Sequence 50 BP; 21 A; 9 C; 10 G; 10 T; 0 other;  
 SQ Query Match 14.5%; Score 17.4; DB 23; Length 50;  
 Best Local Similarity 68.6%; Pred. No. 1.3e+04;  
 Matches 24; Conservative 0; Mismatches 11; Indels 0; Caps 0;  
 QY 54 GATTGAGGGTTCAGCGCTTCTCTGAAATGATCGA 88  
 DB 43 GTTTCAGTATGATCTGCTTTCTTCTGAAATGATCGA 9  
 RESULT 17  
 AAV58151/c  
 ID AAV58151 standard; DNA: 35 BP.  
 XX AAV58151.  
 AC AAV58151.  
 XX 25-NOV-1998 (first entry)  
 DT Cmr PCR primer designated 3595 from WO9838298 Example 4.  
 DE PCR primer: multiple DNA fragment assembly; complementary overhang;  
 XX annealing; specific; spontaneous; ss.  
 KW Synthetic.  
 OS WO9838298-A1.  
 PN 03-SEP-1998.  
 PD 26-FEB-1998; 98WO-1L00096.  
 PF 27-FEB-1997; 97IL-0120339.  
 PR (GESH-) GESHER-ISRAEL ADVANCED BIOTECS 1996 LTD.  
 PA

XX Sharon G;  
 PI WPI: 1998-481200/41.  
 DR Assembling DNA fragments - using complementary overhangs longer than  
 PT 14 bp to obtain high rates of annealing  
 XX Example 4: Page 41; 53pp; English.  
 PS A method has been developed for the high efficiency assembling of  
 CC multiple DNA fragments. The method comprises: (1) providing each  
 CC fragment with at least one overhang that is: (a) capable of hydrogen  
 CC bonding to a complementary sequence on a second fragment; and (b) at  
 CC least 15 bases long; and (ii) mixing the fragments under conditions that  
 CC will promote joining. Also described are: (1) a DNA fragment with either  
 CC an overhang of at least 15 bases, or an end portion suitable for  
 CC conversion to such an overhang; and (2) a DNA construct prepared by the  
 CC above method. AAV58119 to AAV58168 are PCR primers used in the method of  
 CC the invention. In examples shown in the present invention, increasing  
 CC the length of the overhang from 12 bases (prior art) to 15 results in a  
 CC dramatic increase in annealing efficiency and specificity. This allows  
 CC the ratio of reagents to be reduced from 1:100-300 to about 1:1, and  
 CC permits multiple fragments (three or more) to simultaneously join  
 CC together in a directional, predetermined way. The invention is much more  
 CC efficient than prior art techniques, producing a higher yield in a  
 CC shorter length of time.  
 XX Sequence 35 BP; 17 A; 4 C; 9 G; 5 T; 0 other;  
 SQ Query Match 14.3%; Score 17.2; DB 19; Length 35;  
 Best Local Similarity 73.3%; Pred. No. 1.4e+04;  
 Matches 22; Conservative 0; Mismatches 8; Indels 0; Caps 0;  
 QY 89 TTGCTTCCATGCTGCTGATTCGATTT 118  
 DB 31 TTGCTTCCATGCTGCTGATTCGATTT 2  
 RESULT 18  
 AAV58098/c  
 ID AAV58098 standard; DNA: 35 BP.  
 XX AAV58098.  
 AC AAV58098.  
 XX 24-NOV-1998 (first entry)  
 DT PCR primer designated 3595 from WO9838297 Example 1.  
 DE PCR primer: multiple DNA fragment single step assembly; promoter;  
 KW regulatory function; simultaneous assembly; genetic engineering;  
 KW construct; ss.  
 OS Synthetic.  
 XX WO9838297-A1.  
 PN 03-SEP-1998.  
 PD 26-FEB-1998; 98WO-1L00095.  
 PF 27-FEB-1997; 97IL-0120338.  
 PR (GESH-) GESHER-ISRAEL ADVANCED BIOTECS 1996 LTD.  
 PA Sharon G;  
 PI WPI: 1998-481195/41.  
 DR Single step assembly of multiple DNA fragments - useful to join  
 PT fragments with regulatory function e.g. promoters, and fragments  
 PT encoding proteins to produce constructs for genetic engineering  
 XX

Example 1: Page 40; 89pp; English.

XX A method has been developed for the simultaneous assembly of two or more  
XX double-stranded DNA fragments, particularly fragments produced by primer  
XX extension reaction and especially by PCR or by restriction cleavage.  
XX AAV58074 to AAV58118 are PCR primers for use in the method of the  
XX invention, and which are used in examples in the present invention. The  
XX method can be used to join DNA fragments having a regulatory function  
XX (e.g. promoters, enhancers, terminators or ribosome binding sites) and  
XX fragments encoding proteins e.g. enzymes (especially citrate synthases,  
XX polyketide synthases and succinyl-CoA-synthetase), cytokines or  
XX hormones. Constructs produced are useful in genetic engineering e.g. a  
XX new promoter may be attached to a DNA fragment encoding a protein to  
XX produce a new construct in which the protein is under the control of the  
XX promoter, or new chimeric promoters or proteins produced, and such  
XX constructs expressed in host cells. One or more of the fragments may be a  
XX mutant fragment which has been subjected to site-directed mutagenesis or  
XX mutagenic PCR e.g. to improve the activity of a promoter or protein to be  
XX expressed. The method also allows the improvement of joining multiple DNA  
XX fragments in a directional manner, since joining via a ss  
XX step there is no unwanted linker between joined fragments (i.e. joining  
XX is seamless), and (unlike in previous methods) three or more fragments  
XX can be joined efficiently.

XX Sequence 35 BP: 17 A; 4 C; 9 G; 5 T; 0 other:

Query Match 14.3% Score 17.2; DB 19; Length 35;  
Best Local Similarity 73.3%; Pred. No. 1.4e+04;  
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 89 TTGGCTTCATAGCTGCTGAATTCAGTTT 118  
DB 31 TTAGCTTCCTAGCTGCTGATTCATGTT 2

RESULT 19

AAV58077/c  
ID AAV58077 standard; DNA: 35 BP.

XX AAV58077;

XX 24-NOV-1998 (first entry)

XX PCR primer designated 35972 from WO9838296 Example 1.

XX PCR primer; simultaneous ligation; multiple DNA fragment; assembly;  
XX primer extension generated double stranded DNA fragment; UDG;  
XX uracil DNA glycosylase; one-step multiple DNA fragment cloning method;  
XX du residue; apurinate; ss.

XX Synthetic.

XX Key Location/Qualifiers  
XX misc\_RNA 20  
XX /\*tag= a

XX WO9838296-A1.

XX 03-SEP-1998.

XX 26-FEB-1998; 98WO-IL00094.

XX 27-FEB-1997; 97IL-0120337.

XX (GESH-) GESH-ISR-ADVANCED BIOTECS 1996 LTD.

XX Sharon G.

XX WPI: 1998-481198/A1.

XX Novel one-step method for cloning multiple DNA fragments - uses  
XX primers containing an apurinated site for generating single strand  
XX nick followed by dissociation to produce annealable overhangs

Example 1: Page 30; 77pp; English.

XX A method has been developed of ligating 2 or more double stranded DNA  
XX molecules produced e.g. by PCR. The method comprises: (i) providing a  
XX pair of primers complementary to each end of the DNA molecule where the  
XX primers may also be partially complementary to a second and/or third  
XX molecule and each primer contains a deoxy-uracil (dU) residue replacing  
XX a deoxy-thymine (dT) residue at least 15 nucleotides from the 5' end  
XX of the primer; (ii) annealing the primer and extending the DNA fragment  
XX by a primer extension reaction; (iii) adding UDG (uracil DNA  
XX glycosylase) to apurinate the dU residue, and a second enzyme or compound  
XX e.g. N,N-dimethylbenzylamine, to generate single strand nicks at the  
XX apurinated dU residue; (iv) dissociating the nicked oligonucleotides  
XX from the extended fragments; (v) allowing the extended fragments to  
XX anneal to a second or third fragment and ligating them to generate a  
XX multi-DNA fragment assembly product. AAV58076 to AAV58093 are PCR  
XX primers used in the method of the invention. Examples of the present  
XX invention are described below. The method allows the directional joining of  
XX 2 or more double stranded DNA fragments. The method avoids the time  
XX consuming checking procedures required after each cloning step in the  
XX generation of the construct.

XX Sequence 35 BP: 17 A; 4 C; 9 G; 4 T; 1 U; 0 other:

Query Match 14.3% Score 17.2; DB 19; Length 35;  
Best Local Similarity 73.3%; Pred. No. 1.4e+04;  
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 89 TTGGCTTCATAGCTGCTGAATTCAGTTT 118  
DB 31 TTAGCTTCCTAGCTGCTGATTCATGTT 2

RESULT 20

AAV58173/c  
ID AAV58173 standard; DNA: 35 BP.

XX AAV58173;

XX 24-NOV-1998 (first entry)

XX PCR primer designated 3595 from WO9838299 Example 1.

XX PCR primer; multiple DNA fragment single step assembly; construct;  
XX complementary overhang; simultaneous multi-DNA assembly; hormone;  
XX cytokine; enzyme; ss.

XX Synthetic.

XX WO9838299-A1.

XX 03-SEP-1998.

XX 26-FEB-1998; 98WO-IL00097.

XX 27-FEB-1997; 97IL-0120338.

XX (GESH-) GESH-ISR-ADVANCED BIOTECS 1996 LTD.

XX Sharon G.

XX WPI: 1998-481201/A1.

XX Single step directional assembly of multiple DNA fragments - using  
XX complementary overhangs to produce joined DNA with no linker in  
XX between; for expressing e.g. hormones, cytokine(s), enzymes

XX Example 1: Page 38; 73pp; English.

XX A method has been developed for the simultaneous multi-DNA assembly of  
XX at least 2 double-stranded DNA fragments produced by primer extension  
XX reaction, especially the polymerase chain reaction (PCR), or by







PA (ISIS-) ISIS PHARM INC.  
 PI Ward DT, Gaarde WA, Monia BP, Wyatt JR;  
 XX WPI: 2002-416486/44.  
 XX New antisense compound targeted to nucleic acid encoding  
 PT mitogen-activated protein kinase 4, useful for treating immunologic  
 PT disorder, inflammatory disorder or cancer  
 XX Example 15: Page 93; 133pp: English.  
 CC The present invention relates to antisense compounds, compositions and  
 CC methods for modulating the expression of MEKK4 (also referred as mitogen-  
 CC activated protein kinase 4; MAP3K4; MAP three kinase 1; MAP/ERK  
 CC kinase kinase 4; MAPKKK4; MKK1). The antisense oligos are useful for  
 CC inhibiting the expression of MEKK4 in cells or tissues. They are also  
 CC useful for treating an animal having a disease or condition associated  
 CC with MEKK4 such as immunological, inflammatory, hyperproliferative  
 CC disorder or cancer. Sequences of the invention are also useful for  
 CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.  
 CC They are also useful in antisense therapy. The present sequence is an  
 CC antisense oligonucleotide targeted to human MEKK4 DNA. This sequence  
 CC is used in the exemplification of the invention.  
 XX Sequence 20 BP: 3 A: 5 C: 6 G: 6 T: 0 other;  
 SQ Query Match 14.2%; Score 17: DB 24; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 44 ACTCCAGAGGATTTCAG 60  
 DB (20 ACTCCAGAGGATTTCAG 4  
 RESULT 25  
 ID AAO93302/C  
 XX AAO93302 standard: RNA; 30 BP.  
 AC AAO93302;  
 XX 14-AUG-1996 (first entry)  
 DE Two member family bFGF 2'-NH2 RNA ligand 55A.  
 KW Family 1: family 2: ligand; basic fibroblast growth factor; bFGF;  
 KW systematic evolution of ligands by exponential enrichment; SELEX;  
 KW heparin; selection; region of homology; inhibitor; ss.  
 XX Synthetic.  
 OS Key Location/Qualifiers  
 FH modified\_base 1..30  
 FT /\*tag= a  
 FT /mod\_base= c = 2'-NH2 cytosine  
 FT /mod\_base= u = 2'-NH2 uracil  
 XX WO9521853-A1.  
 XX 17-AUG-1995.  
 XX 06-FEB-1995; 95WO-0501458.  
 XX 28-MAR-1994; 94US-0219012.  
 XX 10-FEB-1994; 94US-0195005.  
 XX 11-JUN-1990; 90US-0536428.  
 XX 10-JUN-1991; 91US-0714131.  
 XX 22-APR-1993; 93US-0061691.  
 XX (NEXS-) NEXSTAR PHARM INC.  
 PA Gold L, Janjic N, Tasset D;  
 PI Novel nucleic acid ligands to basic fibroblast growth factor that are

XX WPI: 1995-293073/38.  
 XX Identification of ligands to basic fibroblast growth factor and  
 PT thrombin - which can be modified for increased in vivo stability  
 XX Claim 17: Page 85; 236pp: English.  
 XX The sequences given in AAO93258-342 represent a group of 2'-NH2 RNA  
 CC ligands to basic fibroblast growth factor (bFGF). These sequences  
 CC represent the fragment in the consensus sequence given in AAO93345.  
 CC These ligands were isolated using systematic evolution of ligands by  
 CC exponential enrichment (SELEX). The selection was conducted in PBS  
 CC at 37 deg. C in the presence of heparin which competes with the RNA  
 CC for binding to bFGF. The starting ligand pools contained 2'-NH2  
 CC modified RNA which has improved stability. After twelve rounds of  
 CC selection, the RNA pools showed a definite departure from randomness.  
 CC the affinity of the modified RNA pools was improved by 1-2 orders of  
 CC magnitude. Individual members of the enriched pools were then cloned  
 CC into pUC18 and sequenced. Distinct families were identified based on  
 CC overlapping regions of homology (see also AAO93258-95). A number of  
 CC sequences showed homology to two families (see also AAO93296-303) and  
 CC some sequences showed no obvious homology to any of the families  
 CC (see also AAO93304-22). One family of ligands bound nitrocellulose  
 CC (see also AAO93323-42). These ligands are inhibitors of bFGF and are  
 CC therefore useful in treating bFGF mediated conditions and in studying  
 CC the structure and binding of bFGF.  
 XX Sequence 30 BP: 6 A: 2 C: 16 G: 6 U: 0 other;  
 SQ Query Match 14.2%; Score 17: DB 16; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 16 CCTCTTAACCCACACC 32  
 DB 29 CCTCTTAACCCACACC 13  
 RESULT 26  
 ID AAF70683/C  
 XX AAF70683 standard: RNA; 30 BP.  
 AC AAF70683;  
 XX 20-APR-2001 (first entry)  
 DE 2'-NH2 RNA ligand to bFGF #45.  
 KW Ligand; basic fibroblast growth factor; bFGF; gene therapy; vascular;  
 KW atherosclerosis; angioplasty; stability; ss.  
 XX Unidentified.  
 OS US6177557-A1.  
 XX 23-JAN-2001.  
 XX 05-AUG-1996; 96US-0687421.  
 XX 11-JUN-1990; 90US-0536428.  
 XX 10-JUN-1991; 91US-0714131.  
 XX 06-NOV-1992; 92US-0973333.  
 XX 10-FEB-1994; 94US-0195005.  
 XX 28-MAR-1994; 94US-0219012.  
 XX (NEXS-) NEXSTAR PHARM INC.  
 PA Janjic N, Gold L, Tasset D;  
 PI Novel nucleic acid ligands to basic fibroblast growth factor that are

PT useful as inhibitors of basic fibroblast growth factors and 2'-amino  
XX modified RNA ligands, exhibit increased in vivo stability.

PS Claim 2: Column 49-50: 153pp; English.

XX The present invention relates to a purified and isolated non-naturally  
CC occurring DNA ligands to basic fibroblast growth factor (bFGF).  
CC The ligands are useful as part of gene therapy treatments and  
CC for diagnosing pathogenesis of vascular diseases including  
CC initiation and progression of atherosclerosis, acute coronary  
CC syndromes, vein graft disease and restenosis following coronary  
CC angioplasty. The ligands have improved stability in vivo.

XX Sequence 30 BP: 6 A; 2 C; 16 G; 6 U; 0 other;

Query Match 14.2%; Score 17; DB 22; Length 30;

Best Local Similarity 100.0%; Pred. No. 1.5e+04;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 CCCTCTTAACCCACACC 32

DB 29 CCCTCTTAACCCACACC 13

#### RESULT 27

ID AAZ27695/C

XX AAZ27695 standard; DNA: 32 BP.

XX AAZ27695;

XX 22-DEC-1999 (first entry)

XX PCR primer for verotoxin gene.

XX Verotoxin; VTL; VT2; detection; PCR primer: 59.

XX Synthetic.

XX Escherichia coli.

XX JP11243996-A.

XX 14-SEP-1999.

XX 27-FEB-1998; 98JP-0047677.

XX 27-FEB-1998; 98JP-0047677.

XX (TOYM) TOYOBO KK.

XX WPI: 1999-603716/52.

XX An oligonucleotide for amplification of verotoxin - useful in the  
XX detection of inactivated verotoxin gene by transfer of a foreign DNA  
XX fragment

XX Claim 12: Page 10; 10pp; Japanese.

XX This sequence represents a PCR primer of the invention. The primer is  
XX used for amplification of the E. coli verotoxin (VT) gene. The  
XX oligonucleotide is useful for detection of inactivated VT gene by  
XX transfer of a foreign DNA fragment. Simple, rapid and specific  
XX amplification of VT gene from environmental factors is achieved using the  
XX oligonucleotide of the invention.

XX Sequence 32 BP: 10 A; 9 C; 6 G; 7 T; 0 other;

Query Match 14.2%; Score 17; DB 20; Length 32;

Best Local Similarity 80.0%; Pred. No. 1.5e+04;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 95 TCCATAGCTGCTGATTCAGTTTA 119

DB 26 TCCGATTTGCTGATTCAGTTTA 2

#### RESULT 28

ID ABN86086

XX ABN86086 standard; DNA: 33 BP.

XX ABN86086;

XX 02-OCT-2002 (first entry)

XX Human caudal action protein 17.38 related primer 4.

XX Human; Caudal action protein 17.38; protein metabolism disorder; PCR;

XX primer: 58.

XX Homo sapiens.

XX CN1340534-A.

XX 20-MAR-2002.

XX 31-AUG-2000; 2000CN-0119801.

XX 31-AUG-2000; 2000CN-0119801.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI: 2002-436428/47.

XX Human caudal action protein 17.38 and encoding polynucleotide, useful

XX for treating protein metabolism disorder.

XX Example 4: Page 18 (disclosure); 33pp; Chinese.

XX The invention relates to a human caudal action protein 17.38, the

XX encoding polynucleotide and a method for preparing the polypeptide by DNA

XX recombination techniques. The polypeptide is used in treating diseases

XX such as protein metabolism disorder. The current sequence represents a

XX human caudal action protein 17.38 related primer sequence.

XX Sequence 33 BP: 7 A; 9 C; 9 G; 8 T; 0 other;

Query Match 14.2%; Score 17; DB 24; Length 33;

Best Local Similarity 80.0%; Pred. No. 1.6e+04;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 46 TCCAGAGGATTCAGGGGTTCCAGC 70

DB 7 TCCTCAGTCATCCAGGTTTCCAGC 31

#### RESULT 29

ID AAX58315

XX AAX58315 standard; DNA: 48 BP.

XX AAX58315;

XX 02-AUG-1999 (first entry)

XX Human Toll protein PRO358 hybridisation probe 2.

XX PRO358; Toll; homologue; human; adaptive immunity; septic shock;

XX pathogen pattern recognition receptor; hybridisation; probe: 58.

XX Synthetic

XX Homo sapiens.

XX WO9920756-A2.

XX 29-APR-1999.

PF 07-OCT-1998; 98WO-US21141.  
 XX 26-JUN-1998; 98US-0105413.  
 PR 17-OCT-1997; 97US-0062250.  
 PR 13-NOV-1997; 97US-0065311.  
 PR 28-APR-1998; 98US-0083322.  
 PR 26-JUN-1998; 98US-0090863.  
 XX (GENTH) GENENTECH INC.  
 XX Goddard A, Godowski PJ, Gurney AL, Mark MR, Yang R;  
 DR WPI: 1999-302739/25.  
 XX New human Toll-like receptors that recognize microbial structures  
 XX Example 12: Page 55; 79pp: English.  
 XX This oligonucleotide is one of two probes (see also AAX58314) used  
 CC to examine the expression pattern of PRO358 (see AAY05868), a novel  
 CC human homologue of Drosophila toll protein that acts as a pathogen  
 CC pattern recognition receptor. The probe is based on full-length  
 CC DNA7361 (see AAX58297). Expression was found in gut-associated  
 CC lymphoid tissue and developing splenic white pulp in the foetus.  
 CC Low level expression was seen in the PALS region of normal adult  
 CC spleen. All other tissues were negative. Isolated nucleic acids  
 CC encoding PRO357 polypeptides, a process for producing PRO358  
 CC polypeptides and an antibody which specifically binds to a PRO358  
 CC polypeptide are claimed. The antibody is used in a claimed method  
 CC for the treatment of septic shock.  
 XX Sequence 48 BP; 12 A; 7 C; 11 G; 18 T; 0 other;  
 SQ

Query Match 14.0%; Score 17; DB 20; Length 48;  
 Best Local Similarity 69.7%; Pred. NO. 1.8e+04;  
 Matches 23; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 41 CCCACTCAGAGGATTCAGGGTTCACGCGTT 73  
 DB 13 CCCTCACTAAGGAGGATTCAGTTCTCTGGGTT 45

RESULT 30  
 AAZ23112/C  
 ID AAZ23112 standard; DNA; 30 BP.  
 XX AAZ23112;  
 XX 17-JAN-2000 (first entry)  
 XX Human CD4 transgene hybridizing internal probe.  
 XX Transgenic rat; lentiviral; LV; HIV infection; AIDS; primate; HIV-1;  
 XX HIV-2; simian immunodeficiency virus; SIV; feline immunodeficiency virus;  
 XX FIV; bovine immunodeficiency virus; BIV; CAEV; EIAV; CD4 gene; Probe;  
 XX Caprine arthritis encephalitis virus; equine infectious anemia virus; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO952349-A1.  
 XX 21-OCT-1999.  
 XX 09-APR-1999; 99WO-US07621.  
 XX 09-APR-1998; 98US-0058113.  
 XX (UYMA-) UNIV MARYLAND CONSTITUENT INST.  
 XX Bryant JL, Reid WC, Davis HG, Flannand L;  
 XX WPI: 1999-620240/53.

XX New transgenic rats containing lentiviral nucleic acid, used for  
 PT developing products for treating or preventing lentivirus infection,  
 PT particularly HIV infection  
 XX Example 5; Page 38; 57pp: English.  
 XX The invention provides a novel transgenic rat that comprises cells which  
 CC comprise at least one copy of a lentiviral (LV) nucleic acid. The  
 CC transgenic rats can be used as models of LV (e.g. HIV infection and  
 CC development of disease (e.g. AIDS). The LVs also include primate LVs  
 CC e.g. HIV-1/HIV-2, simian immunodeficiency virus (SIV) from chimpanzee  
 CC monkey (SIVcpz), Sooty mangabey (SIVsmm), African Green Monkey (SIVagm), SIV's  
 CC feline immunodeficiency virus (FIV), bovine LVs, e.g. bovine  
 CC immunodeficiency virus (BIV), ovine LVs e.g. Maedi/Vienna virus (MVV) and  
 CC Caprine arthritis encephalitis virus (CAEV), and equine LVs e.g. equine  
 CC infectious anemia virus (EIAV). The animals can be used for identifying  
 CC agents for treating or preventing a disease or condition associated with  
 CC LV. The present sequence represents a probe hybridizing to a human CD4  
 CC transgene fragment.  
 XX Sequence 30 BP; 5 A; 4 C; 16 G; 5 T; 0 other;  
 SQ

Query Match 14.0%; Score 16.8; DB 20; Length 30;  
 Best Local Similarity 75.0%; Pred. NO. 1.8e+04;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 24 ACCGACACCTCATTTATCCCACTCCAGA 51  
 DB 29 ACCGACACCGCTTCTCCGCTTCGAGA 2

RESULT 31  
 AAV67934/C  
 ID AAV67934 standard; DNA; 31 BP.  
 XX AAV67934;  
 XX 24-DEC-1998 (first entry)  
 XX Nucleotide fragment containing polymorphic site, WI-12345.  
 XX ss; polymorphic site; nucleic acid analysis; diagnosis; monitoring;  
 XX cancer; inflammation; heart disease; CNS disease.  
 XX Homo sapiens.  
 XX WO9838846-A2.  
 XX 11-SEP-1998.  
 XX 06-MAR-1998; 98WO-US04571.  
 XX 28-MAR-1997; 97US-0042125.  
 XX 07-MAR-1997; 97US-0813159.  
 XX (AFFY-) AFFYMETRIX INC.  
 XX Berno A, Chee M, Fan J, Lipshutz RJ;  
 XX WPI: 1998-495419/42.  
 XX New nucleic acid segments containing polymorphic sites, or  
 PT complements and methods of detecting a nucleic acid for general  
 PT use including diagnosis and monitoring of diseases  
 XX Claim 1; Page 28; 42pp: English.  
 XX New nucleic acid segment comprising one of the 10 - 100 bp sequences  
 CC given in the specification (sequences of a polymorphic site), or the  
 CC complement of the segment and a method of analysing a nucleic acid  
 CC comprising determining the base occupying the polymorphic site of the



```

RESULT 34
AAZ66282
ID AAZ66282 standard; DNA: 47 BP.
XX
AC AAZ66282;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:629.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(24,C)
FT /*tag= a
FT /*standard_name= "single nucleotide polymorphism"
XX
PN WO954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99MO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI: 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome
XX
PS Claim 1: Page 364; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 15 A; 9 C; 14 G; 9 T; 0 other;
XX
Query Match 14.0%; Score 16.8; DB 21; Length 47;
Best Local Similarity 61.4%; Pred. No. 2.1e+04;
Matches 27; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
XX
OY 46 TCCAGAGGATTCAGGGGTTCCAGGCTTCCTGAAATGATCGAT 89
| | | | | | | | | | | | | | | | | | | | |
DB 3 TACAGAGAATTCATGTGTGTCATGAGACCCAGGACATGGCCGAT 46
| | | | | | | | | | | | | | | | | | | | |
RESULT 35
AAZ67660
ID AAZ67660 standard; DNA: 47 BP.
XX
AC AAZ67660;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:2007.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(24,C)
FT /*tag= a
FT /*standard_name= "single nucleotide polymorphism"
XX
PN WO954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99MO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI: 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome
XX
PS Claim 1: Page 658; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 15 A; 16 C; 7 G; 9 T; 0 other;
XX
Query Match 14.0%; Score 16.8; DB 21; Length 47;
Best Local Similarity 66.7%; Pred. No. 2.1e+04;
Matches 24; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
XX
OY 20 CCTAACCCACACCTCATTTATCCCTCCCTCCAGAGGCA 55
| | | | | | | | | | | | | | | | | | | | |
DB 2 CATCAAAATGCTCATTTATCCCTCCCTCCAGAGGCA 37
| | | | | | | | | | | | | | | | | | | | |
RESULT 36
AAT33570/C
ID AAT33570 standard; DNA: 40 BP.
XX

```



CC The specification describes a novel method of controlling cell functions  
 CC controlled by the tumour necrosis factor receptor (TNF-R) pathway  
 CC containing U1-70. The method comprises introducing a nucleic acid  
 CC molecule encoding CrmA into a cell, and culturing the cell under  
 CC suitable conditions for transcription and translation of the CrmA  
 CC nucleic acid. Method for preventing and inhibiting apoptosis by  
 CC inhibiting activation of the U1-70 path, identifying the chemical related  
 CC to the apoptosis path, and screening a candidate chemical having  
 CC biological function in the apoptosis path are also described. The methods  
 CC can be used to identify substances which modulate apoptosis in cells  
 CC controlled by the TNF-R pathway.

SQ Sequence 40 BP; 11 A; 6 C; 10 G; 13 T; 0 other;

Query Match 13.8%; Score 16.6; DB 19; Length 40;

Best Local Similarity 64.1%; Pred. No. 2.3e+04;  
 Matches 25; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 14 GACCTCTCTAACCCACACCTCATTTATCCCTCCACTCCAGAG 52

DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

40 GATATGCTCTCAACAACTAATTAACCTGAGTCTAGAG 2

RESULT 39

AAZ67133

ID AAZ67133 standard; DNA: 47 BP.

XX AC AAZ67133;

XX DT 10-SEP-2001 (first entry)

XX DE Human map-related biallelic marker SEQ ID NO:1480.

XX Human genome; biallelic marker; high density disequilibrium map;  
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
 KW haplotyping; hybridisation; identification; characterisation;  
 KW diagnosis; single nucleotide polymorphism; SNP; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT variation replace(24,G)  
 FT /\*tag- a

FT /standard\_name= "single nucleotide polymorphism"

XX PN W09954500-A2.

XX PO 28-OCT-1999.

XX PF 21-APR-1999; 99WO-IB00822.

XX PR 21-APR-1998; 98US-0082614.

XX PR 23-NOV-1998; 98US-0109732.

XX PA (GEST ) GENSET.

XX PI Cohen D, Blumenfeld M, Chumakov I;

XX DR WPI: 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium  
 PT map of the human genome

XX Claim 1: Page 546; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present  
 CC invention, which contain a polymorphic base at position 24 of their  
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
 CC primers for the biallelic markers. The biallelic markers of the  
 CC invention have a variety of uses: they can be used for high density  
 CC mapping of the human genome, and in complex association studies and  
 CC haplotyping studies which are useful in determining the genetic basis  
 CC for disease states. Compositions and methods of the invention can also

CC be useful for the identification of the targets for the development of  
 CC pharmaceutical agents and diagnostic methods, as well as the  
 CC characterisation of the differential efficacious responses to and side  
 CC effects from pharmaceutical agents acting on a disease as well as other  
 CC treatment.  
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297  
 CC and 3367, are not actually given a sequence in the Sequence Listing  
 CC from the present invention.

SQ Sequence 47 BP; 13 A; 15 C; 6 G; 13 T; 0 other;

Query Match 13.8%; Score 16.6; DB 21; Length 47;

Best Local Similarity 64.1%; Pred. No. 2.5e+04;

Matches 25; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 13 TGACCTCTCTAACCCACACCTCATTTATCCCTCCACTCCAGA 51

DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

7 TGCACTTTCTGCCCAAGACCTCTGTATTACATTACAGA 45

RESULT 40

ABK40897/c

ID ABK40897 standard; DNA: 47 BP.

XX AC ABK40897;

XX DT 21-MAY-2002 (first entry)

XX DE Human obesity-associated chromosome 10 biallelic marker #105.

XX Human; obesity associated-biallelic marker; chromosome 10; obesity; ds;  
 KW drug response; hyperuricaemia; digestive pathology; hypertension; cancer;  
 KW hepatic function disorder; cardiovascular disease; hyperlipidaemia;  
 KW insulin disorder; atheromatous disease; cardiac insufficiency.

XX OS Homo sapiens.

XX PN W0200206525-A2.

XX PD 24-JAN-2002.

XX PF 28-JUN-2001; 2001WO-IB01477.

XX PR 18-JUL-2000; 2000US-219704P.

XX PA (GEST ) GENSET.

XX PI Cohen D, Blumenfeld M, Chumakov I, Abderrahim H, Bihaïn B;

XX DR WPI: 2002-155043/20.

XX Set of novel map-related biallelic markers, preferably located on  
 PT obesity disorder-associated chromosomal regions on chromosomes 3, 10  
 PT and 19, useful, for e.g. detecting statistical correlations between  
 PT marker allele and a phenotype

XX Claim 1: Page 222; 311pp; English.

XX The invention relates to a set of novel map-related biallelic markers,  
 CC preferably located on obesity disorder-associated chromosomal regions on  
 CC chromosomes 3, 10 and 19. The markers are useful for genotyping or  
 CC estimating the frequency of an allele in a population, for detecting an  
 CC association between a genotype or haplotype and a phenotype, e.g. a  
 CC disease involving drug responses, obesity or disorders related to  
 CC obesity, such as hyperuricaemia, digestive pathology, hepatic function  
 CC disorders, cancer, cardiovascular disease, hypertension, hyperlipidaemia,  
 CC insulin disorders, atheromatous disease and cardiac insufficiency. The  
 CC markers are useful for detecting a statistical correlation between a  
 CC biallelic marker allele and a phenotype and/or between a biallelic marker  
 CC haplotype and a phenotype. This sequence represents a human  
 CC obesity-associated biallelic marker located on chromosome 10.

SQ Sequence 47 BP; 17 A; 9 C; 11 T; 1 other;







[illegible]

XX 21-DEC-1998; 98CN-0125687.  
 XX (UYFO-)} UNIV FUDAN.  
 XX Yu L, Jiang C, Fu Q;  
 XX WPI: 2000-544295/50.  
 XX Cytokine signal transfer arrestin IV -  
 XX  
 XX Example 3; Page 10; 16pp; Chinese.  
 XX  
 XX The invention relates to human cytokine signal transfer arrestin IV  
 CC (B23177), to cDNA encoding it (A97467), and to the recombinant production  
 CC of human cytokine signal transfer arrestin IV. Human cytokine signal  
 CC transfer arrestin IV is a member of the cytokine inducible SH2-containing  
 CC protein (CIS) family and is a close homologue of SOCS-4 (suppressor of  
 CC cytokine signalling; GenBank Accession No. AF035947). The gene  
 CC encoding human cytokine signal transfer arrestin IV is located on  
 CC chromosome 3p21.3. Sequences A97472-A97473 represent PCR primers  
 CC used in an exemplification of the invention to subclone human cytokine  
 CC signal transfer arrestin IV cDNA.  
 XX  
 XX Sequence 29 BP; 5 A; 10 C; 7 G; 7 T; 0 other;  
 SQ  
 Query Match 13.5%; Score 16.2; DB 21; Length 29;  
 Best Local Similarity 72.4%; Pred. No. 2.9e+04;  
 Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 49 AGAGGGATTCAGGGTTCAGGCTTCCTG 77  
 DB 1 AGATGGATTCAGGGTTCAGGCTTCCTG 29  
 RESULT 48  
 AAV27067  
 ID AAV27067 standard; DNA; 32 BP.  
 XX  
 AC AAV27067;  
 XX  
 DT 16-SEP-1998 (first entry)  
 XX  
 DE Double-stranded adenosine deaminase 88 kD protein antisense primer.  
 XX  
 KW ss: Human; double-stranded adenosine deaminase; neurological disorder;  
 KW CNS disorder; PCR: primer: amplification.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN US576374-A.  
 XX  
 PD 09-JUN-1998.  
 XX  
 PF 13-NOV-1994; 9405-0555678.  
 XX  
 PR 13-NOV-1995; 9505-0555678.  
 PR 17-FEB-1994; 9405-0157794.  
 PR 25-JUL-1984; 9405-0280443.  
 PR 01-JUN-1995; 9505-0457459.  
 XX  
 XX (WIST-)} WISTAR INST ANATOMY & BIOLOGY.  
 XX  
 XX Nishikura K;  
 XX  
 XX WPI: 1998-347307/30.  
 XX  
 XX Diagnosis of disorders characterised by inappropriate expression of  
 PT enzyme; comprises contacting tissue sample with labelled  
 PT antibodies, oligonucleotides or protein reagent and measuring  
 PT association of enzyme  
 XX

PS Example 3; Column 14; 66pp; English.  
 XX  
 CC The primers AAV27066 and AAV27067 and the probe AAV27069 were used to  
 CC identify the 88 kD double-stranded adenosine deaminase protein. Which is  
 CC one of two fragments of the 140 kD protein encoded by the  
 CC double-stranded adenosine deaminase gene. The other protein being a  
 CC fragment of 93 kD; both proteins have similar biological activity to the  
 CC full length protein. Double-stranded adenosine deaminase is specific  
 CC for double-stranded RNA and is useful for the diagnosis of disorders  
 CC characterised by inappropriate double-stranded ribonucleic acid  
 CC adenosine deaminase expression. Particularly for diagnosis of certain  
 CC neurological or CNS disorders, e.g. Alzheimer's disease, Huntington's  
 CC disease, subacute sclerosing panencephalitis, measles inclusion body  
 CC encephalitis or stroke, or other neurological conditions associated with  
 CC aging.  
 XX  
 XX Sequence 32 BP; 7 A; 7 C; 10 G; 7 T; 1 other;  
 SQ  
 Query Match 13.5%; Score 16.2; DB 19; Length 32;  
 Best Local Similarity 70.0%; Pred. No. 3e+04;  
 Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 60 GGGGTTCCAGCGTTCCTCAAAATGATCGAT 89  
 DB 2 GGGATCCGATCGATCGGTAATGATCGAT 31  
 RESULT 49  
 AAT42149  
 ID AAT42149 standard; DNA; 33 BP.  
 XX  
 AC AAT42149;  
 XX  
 DT 14-MAY-1997 (first entry)  
 XX  
 DE HIV-1 gp120 V3 loop PCR primer.  
 XX  
 KW Human immunodeficiency virus; HIV-1; envelope glycoprotein gp120;  
 KW variable loop; Zaire; acquired immune deficiency syndrome; AIDS;  
 KW vaccine; immunodiagnosis; polymerase chain reaction; PCR; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN FR2730493-A1.  
 XX  
 PD 14-AUG-1996.  
 XX  
 PF 09-FEB-1995; 95FR-0001513.  
 XX  
 PR 09-FEB-1995; 95FR-0001513.  
 XX  
 PA (INSP ) INST PASTEUR.  
 XX  
 XX Chamaret S, Cohen J, Guelard D, Montagnier L, Philbert F;  
 XX Tabary T;  
 XX WPI: 1996-395417/40.  
 XX  
 XX New HIV-1 strain MAD and related nucleic acids and peptide(s) -  
 XX useful for diagnosing HIV-1 infections and generating vaccines  
 XX  
 XX Example; Page 12; 24pp; French.  
 XX  
 XX A new strain of HIV-1 was isolated from a seropositive, asymptomatic  
 CC woman from Zaire; her serum reacted only moderately with peptides  
 CC specific for HIV-1, including subgroup O, and reacted with only one  
 CC African-type V3 peptide. Peptides derived from V3 loops of the new  
 CC HIV-1 strain are useful in vaccines and for immunodiagnosis. The  
 CC present sequence represents an oligonucleotide primer which was used  
 CC for amplifying DNA coding for the V3 loop of HIV-1 envelope  
 CC glycoprotein gp120 from various viral strains. A comparison of  
 CC different strains allowed the immunodominant epitope of HIV-1 MAD  
 CC to be identified.

XX Sequence 33 BP, 11 A; 7 C; 11 G; 4 T; 0 other:  
 SQ Query Match 13.5%; Score 16.2; DB 17; Length 33;  
 Best Local Similarity 85.7%; Pred. No. 3e+04;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 100 ACCTGCTCAATTCGCTTTAG 120  
 ||||| ||||| ||||| ||||| |||||  
 DB 5 ACCTGCAATGCGAGCTAG 25

RESULT 50  
 AAS17068/c  
 ID AAS17068 standard; DNA: 34 BP.  
 XX AC AAS17068;  
 DT 14-FEB-2002 (first entry)  
 XX Transposon-resistant vectors pSAM/p3/7 PCR primer fh204.  
 DE Transposon resistant vector; pSAM; DNA sequencing: p3/7: fh204;  
 KW ss: transposon gammadelta; PCR primer.  
 XX Escherichia coli.  
 OS W020018595-A2.  
 PX 15-NOV-2001.  
 XX 10-MAY-2001: 2001WO-EP05357.  
 XX 10-MAY-2000: 2000EP-0109906.  
 PR (ENBL-) ENBL EURO LAB MOLECULARBIOLOGIE.  
 PA Ansoorge W, Benes V, Hill F;  
 PI MPI; 2002-055601/07.  
 DR New vectors for selective transposon insertion, useful in  
 PT transposon-based DNA sequencing methods, comprises origin of  
 PT replication and selectable marker gene operably linked to promoter  
 PT present in origin of replication.  
 PS Example 1: Page 13: 31pp: English.

XX The invention relates to a vector comprising an origin of replication,  
 CC and a selectable marker gene operably linked to a promoter present in  
 CC the origin of replication, for selective transposon insertion. The  
 CC vector is free of sequences which tolerate transposon insertion. Also  
 CC included is a method of constructing a cloning vector incapable of  
 CC self-ligation comprising linearising the vector, exonuclease degrading  
 CC one strand in a 5'-3' direction to generate a mixture of overlapping  
 CC single-stranded fragments, generating double-stranded versions of  
 CC the fragments using using non-phosphorylated primers, melting the  
 CC double-stranded fragments and then allowing the strands to anneal and  
 CC prime further extension reactions to form a vector lacking 5' phosphates.  
 CC The vector is useful for sequencing nucleic acids. The method comprises  
 CC inserting a nucleic acid to be sequenced (which tolerates transposon  
 CC insertion) into the vector, inserting a transposon containing at least  
 CC two unique primer binding sequences, selecting a recombinant vector  
 CC having a transposon insertion, and sequencing the nucleic acid insert  
 CC using at least two primers capable of binding to the unique sequences.  
 CC The insertion is carried out in a donor host cell, and selection is  
 CC carried out a recipient host cell. The recombinant vector is transferred  
 CC from the donor host cell to the recipient by conjugation, where the  
 CC transposase and/or resolvase enzymes of the transposon are not encoded by  
 CC the transposon but are provided by host cell, more preferably the  
 CC transposase is provided by the donor host cell, where the resolvase is  
 CC provided by the recipient host cell, where the transposase is operatively  
 CC linked to an inducible promoter, preferably arab promoter. The second

CC host cell lacks endonuclease I, recA and carries a selectable resistance  
 CC gene, where the transposon is a class II transposon, preferably  
 CC transposon gammadelta or their derivatives, which is preferably IS102.  
 CC The selectable marker confers resistance in a copy number dependent  
 CC fashion, and insertion is carried out in parallel in several different  
 CC donor host cells comprising different transposons containing different  
 CC unique site for primer binding. The present sequence is a PCR primer used  
 CC to construct the transposon-resistant vectors of the invention, pSAM and  
 CC p3/7, amplifying the chloramphenicol resistance gene.

XX Sequence 34 BP: 13 A; 4 C; 11 G; 6 T; 0 other:  
 SQ Query Match 13.5%; Score 16.2; DB 24; Length 34;  
 Best Local Similarity 85.7%; Pred. No. 3.1e+04;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 89 TTGCTTCATACCTGCTGAA 109  
 ||||| ||||| ||||| ||||| |||||  
 DB 29 TTAGCTTCTTACCTGCTGAA 5

RESULT 51  
 AAV39895  
 ID AAV39895 standard; DNA: 37 BP.  
 XX AC AAV39895;  
 DT 02-OCT-1998 (first entry)  
 XX Streptococcus pneumoniae OMF cloning primer SPQ ID NO:378.  
 DE Streptococcus pneumoniae; antigen: vaccine; infection; diagnosis;  
 KW detection, pneumonia; Otitis media; meningitis; cloning primer; ss.  
 XX Synthetic.  
 OS Streptococcus pneumoniae.  
 PX W05818930-A2.  
 XX 07-MAY-1998.  
 XX 30-OCT-1997; 97WO-US9422.  
 XX 31-OCT-1996; 96US-0025560  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Choi GH, Hromockyj A, Johnson LS, Kunsch CA;  
 PI MPI; 1998-272224/24.  
 XX Nucleic acid encoding antigenic peptide(s) from Streptococcus  
 PT pneumoniae - or their epitope-containing fragments, useful in  
 PT protective or therapeutic vaccines, and for diagnosis  
 PT Example 1: Page 108: 116pp: English.

XX The present sequence represents a cloning primer used in an example from  
 CC the present invention which describes proteins from Streptococcus  
 CC pneumoniae. Nucleic acid sequence encoding Streptococcus pneumoniae  
 CC proteins can be useful in vaccines for inducing protective antibodies  
 CC against Streptococcus pneumoniae, for treatment or prevention of  
 CC infection e.g. pneumonia, otitis media or meningitis. Probes based on  
 CC the nucleic acids are used to detect Streptococcus infection (by usual  
 CC hybridisation or amplification methods), also for isolating  
 CC Streptococcus genes or their allelic variants. The proteins can be used  
 CC similarly to detect specific antibodies in standard immunoassays,  
 CC especially for diagnosing or monitoring infections. Antibodies which  
 CC bind the proteins are used to detect corresponding antigens, to purify  
 CC the proteins and for passive immunisation (optionally coupled to a  
 CC toxin). Vaccines are administered, e.g. by injection, orally or through  
 CC the skin, typically at 0.01-1000 (especially 10-300) µg/g/ml per dose.  
 CC The cloning primers used in the present invention are given in AAV27437



XX SQ Sequence 40 BP; 11 A; 12 C; 10 G; 7 U; 0 other:  
 Query Match 13.5% Score 16.2; DB 17; Length 40;  
 Best Local Similarity 61.9%; Pred. No. 3.2e+04;  
 Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 92 GCTTCATAGCTGCTGATG 112  
 ||||| ||||| ||||| |||||  
 DB 10 GCUCGAAAGCUGGUAUCG 30

RESULT 54  
 AAV25804/c  
 ID AAV25804 standard: RNA; 41 BP.  
 AC AAV25804;  
 DT 10-JUL-1998 (first entry)  
 DE Mutant CATVI.2.5 gene initiation region.  
 KW Protein synthesis: in vivo; VALRS gene; E.coli; haemoglobin;  
 KW somatotropin; CAT gene; initiation region; ss.  
 OS Synthetic.  
 OS Escherichia coli.  
 PX W09808959-A1.  
 PX 05-MAR-1998.  
 PX 28-AUG-1997; 97MO-US15204.  
 PX 29-AUG-1996; 96US-0705196.  
 PX (NAST) MASSACHUSETTS INST TECHNOLOGY.  
 PX Rajbhandary UL.  
 PX WPI: 1998-179444/16.  
 Over-production of protein that does not begin with methionine in  
 cells - that contain DNA encoding the protein, mutant initiator  
 transfer RNA and methionyl-tRNA transferase, particularly for  
 haemoglobin and somatotropin production  
 Disclosure: Fig 2B: 28pp; English.

XX The present sequence represents the initiation region of a CAT gene, used  
 in the present invention. The present invention describes a method for  
 overproducing a protein (I) that has an N-terminal amino acid (aa) other  
 than Met. The method comprises introducing into cells DNA (II) encoding  
 (I) and having a first codon other than that for Met; (II) DNA (III)  
 encoding a mutant initiator transfer RNA containing the appropriate  
 anti-codon and (III) DNA (IV) encoding Met-tRNA transferase (V). The  
 cells are then maintained under conditions that allow overproduction of  
 (V) and expression of (II). Also described are (I) produced this way.  
 (I) is initiated by Val, Ile or Phe. The host cell is Escherichia coli  
 and may also be transformed with DNA (VI) encoding the appropriate  
 aminoacyl tRNA synthetase (VII), which is also overproduced, particularly  
 where Val is the first amino acid. The method is particularly used to  
 produce haemoglobin and somatotropin, or other (I) that are toxic to the  
 producing cells. The combination of mutant initiator tRNA and (II)  
 provides more (I) than wild-type initiator tRNA and wild-type gene,  
 particularly a 5-6 fold increase.

XX Sequence 41 BP; 18 A; 8 C; 8 G; 7 U; 0 other:  
 Query Match 13.5% Score 16.2; DB 19; Length 41;  
 Best Local Similarity 85.7%; Pred. No. 3.3e+04;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 89 TTGCTTCATAGCTGCTGAA 109  
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 DB 22 TTAGCTTCCTTAGCTCTGAA 2

RESULT 55  
 AAV25805/c  
 ID AAV25805 standard: RNA; 41 BP.  
 AC AAV25805;  
 DT 10-JUL-1998 (first entry)  
 DE Mutant CATII.2.5 gene initiation region.  
 KW Protein synthesis: in vivo; VALRS gene; E.coli; haemoglobin;  
 KW somatotropin; CAT gene; initiation region; ss.  
 OS Synthetic.  
 OS Escherichia coli.  
 PX W09808959-A1.  
 PX 05-MAR-1998.  
 PX 28-AUG-1997; 97MO-US15204.  
 PX 29-AUG-1996; 96US-0705196.  
 PX (NAST) MASSACHUSETTS INST TECHNOLOGY.  
 PX Rajbhandary UL.  
 PX WPI: 1998-179444/16.  
 Over-production of protein that does not begin with methionine in  
 cells - that contain DNA encoding the protein, mutant initiator  
 transfer RNA and methionyl-tRNA transferase, particularly for  
 haemoglobin and somatotropin production  
 Disclosure: Fig 2B: 28pp; English.

XX The present sequence represents the initiation region of a CAT gene, used  
 in the present invention. The present invention describes a method for  
 overproducing a protein (I) that has an N-terminal amino acid (aa) other  
 than Met. The method comprises introducing into cells DNA (II) encoding  
 (I) and having a first codon other than that for Met; (II) DNA (III)  
 encoding a mutant initiator transfer RNA containing the appropriate  
 anti-codon and (III) DNA (IV) encoding Met-tRNA transferase (V). The  
 cells are then maintained under conditions that allow overproduction of  
 (V) and expression of (II). Also described are (I) produced this way.  
 (I) is initiated by Val, Ile or Phe. The host cell is Escherichia coli  
 and may also be transformed with DNA (VI) encoding the appropriate  
 aminoacyl tRNA synthetase (VII), which is also overproduced, particularly  
 where Val is the first amino acid. The method is particularly used to  
 produce haemoglobin and somatotropin, or other (I) that are toxic to the  
 producing cells. The combination of mutant initiator tRNA and (II)  
 provides more (I) than wild-type initiator tRNA and wild-type gene,  
 particularly a 5-6 fold increase.

XX Sequence 41 BP; 19 A; 8 C; 7 G; 7 U; 0 other:  
 Query Match 13.5% Score 16.2; DB 19; Length 41;  
 Best Local Similarity 85.7%; Pred. No. 3.3e+04;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 89 TTGCTTCATAGCTGCTGAA 109  
 || ||||| ||||| |||||  
 DB 22 TTAGCTTCCTTAGCTCTGAA 2

RESULT 56  
 AAV25803/c

ID AAV25803 standard; RNA; 41 BP.  
 XX AAV25803;  
 AC  
 XX  
 DT 10-JUL-1998 (first entry)  
 XX  
 DE CAT2.5 gene initiation region.  
 XX  
 KW Protein synthesis; in vivo; VALRS gene; E.coli; haemoglobin;  
 KW somatotropin; CAT gene; initiation region; ss.  
 XX  
 OS Synthetic.  
 OS Escherichia coli.  
 XX  
 PN W09808959-A1.  
 XX  
 PD 05-MAR-1998.  
 XX  
 PF 28-AUG-1997; 97WO-US15204.  
 XX  
 PR 29-AUG-1996; 96US-0705196.  
 XX  
 PA (HASI ) MASSACHUSETTS INST TECHNOLOGY.  
 XX  
 PI Rajbhandary UL;  
 XX  
 DR MPI; 1998-179444/16.  
 XX  
 XX Over-production of protein that does not begin with methionine in  
 PT cells - that contain DNA encoding the protein, mutant initiator  
 PT transfer RNA and methionyl-tRNA transferase, particularly for  
 PT haemoglobin and somatotropin production  
 XX  
 PS Disclosure; Fig 2B; 28pp; English.  
 XX  
 CC The present sequence represents the initiation region of a CAT gene, used  
 CC in the present invention. The present invention describes a method for  
 CC overproducing a protein (I) that has an N-terminal amino acid (aa) other  
 CC than Met. The method comprises introducing into cells DNA (II) encoding  
 CC (I) and having a first codon other than that for Met; (II) DNA (III)  
 CC encoding a mutant initiator transfer RNA containing the appropriate  
 CC anti-codon and (III) DNA (IV) encoding Met-tRNA transferase (V). The  
 CC cells are then maintained under conditions that allow overproduction of  
 CC (V) and expression of (II). Also described are (I) produced this way.  
 CC (I) is initiated by Val, Ile or Phe. The host cell is Escherichia coli  
 CC and may also be transformed with DNA (VI) encoding the appropriate  
 CC aminoacyl tRNA synthetase (VII), which is also overproduced, particularly  
 CC where Val is the first amino acid. The method is particularly used to the  
 CC produce haemoglobin and somatotropin, or other (I) that are toxic to the  
 CC producing cells. The combination of mutant initiator tRNA and (II)  
 CC provides more (I) than wild-type initiator tRNA and wild-type gene,  
 CC particularly a 5-6 fold increase.  
 XX  
 SQ Sequence 41 BP; 19 A; 7 C; 8 G; 7 U; 0 other;  
 Query Match 13.5%; Score 16.2; DB 19; Length 41;  
 Best Local Similarity 85.7%; Pred. No. 3.3e+04;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 89 TTGGCTTCATGCTCTGCA 109  
 DB 22 TTAGCTTCTTAGCTCTGCA 2  
 RESULT 57  
 ABA04577  
 ID ABA04577 standard; DNA; 41 BP.  
 XX  
 AC ABA04577;  
 XX  
 DT 15-FEB-2002 (first entry)  
 XX  
 DE Probe #1.

XX Probe; cytostatic; virucide; immunomodulator; antinflammatory;  
 KW haemostatic; gene therapy; human; tumour; breast cancer; leukaemia;  
 KW kinetic ataxia telangiectasia protein; ATM20; haemopathy; HIV infection;  
 KW ataxia telangiectasia; developmental disorder; immunological disease;  
 KW inflammation; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 PN W0200179426-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 19-MAR-2001; 2001WO-CN00370.  
 XX  
 PR 22-MAR-2000; 2000CN-0115022.  
 XX  
 PA (BIOW-) BIONDOWN GENE DEV INC SHANGHAI.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR MPI; 2002-066355/09.  
 XX  
 XX Human kinetic ataxia telangiectasia protein ATM20 and encoded  
 PT polynucleotide, applicable in diagnosis and treatment of e.g. malignant  
 PT tumor, hemopathy, HIV infection, immunological diseases and various  
 PT inflammations  
 XX  
 PS Example 6; Page 15; 28pp; Chinese.  
 XX  
 CC The present invention relates to a novel human kinetic ataxia  
 CC telangiectasia protein ATM20. ATM20 and its coding sequence are useful  
 CC in the diagnosis and treatment of malignant tumours, e.g. breast cancer  
 CC and leukaemia; haemopathy; HIV infection; ataxia telangiectasia;  
 CC developmental disorders; immunological diseases and various  
 CC inflammations. The present sequence is a probe, which was used in an  
 CC example from the present invention.  
 XX  
 SQ Sequence 41 BP; 12 A; 18 C; 3 G; 8 T; 0 other;  
 Query Match 13.5%; Score 16.2; DB 24; Length 41;  
 Best Local Similarity 85.7%; Pred. No. 3.3e+04;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 20 CCTAACCCACACCTCATTC 40  
 DB 4 CCTACCCCAACCTCATTC 24  
 RESULT 58  
 ABA04578  
 ID ABA04578 standard; DNA; 41 BP.  
 XX  
 AC ABA04578;  
 XX  
 DT 15-FEB-2002 (first entry)  
 XX  
 DE Probe #2.  
 XX  
 KW Probe; cytostatic; virucide; immunomodulator; antinflammatory;  
 KW haemostatic; gene therapy; human; tumour; breast cancer; leukaemia;  
 KW kinetic ataxia telangiectasia protein; ATM20; haemopathy; HIV infection;  
 KW ataxia telangiectasia; developmental disorder; immunological disease;  
 KW inflammation; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 PN W0200179426-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 19-MAR-2001; 2001WO-CN00370.  
 XX





toxic compounds. AAZ34339 to AAZ34450 represent oligonucleotide sequences used in the exemplification of the present invention.

Sequence 45 BP; 13 A; 9 C; 15 G; 7 U; 1 other;

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Query Match	23.5%	Score 16.2;	DB 20;	Length 45;
Best Local Similarity	72.4%	Pred. No. 3.4e+04;		
Matches 21; Conservative	0;	Mismatches 8;	Indels	

[illegible][illegible]

UY I7 UCTFAUCCALACCEICATAIUCCLAL 43

31 CGTCTCACGGACTCATCAGATCCCCAC 3

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RESULTS OF

5/87896VBT |

ID ABA96818

XX  
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AC ABA96878:

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1. The first part of the document is a list of references, which includes the following works:

07-MAY-2002 (first entry)

—

DE Human parathyroid hormone (hPTH) oligonucleotide C3.

—

Human: parathyroid hormone: hPTH: recombinant production:

human, pregnancy hormone, in its recombinant production, VAD2 deficient strain, used as a control.

1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221

KEY *Saccharomyces cerevisiae*; gene construction; ss.

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OS Homo sapiens.

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DN KR99075486-A

33-38610-1

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PD 06-APR-1999.

• **XX**

PF 12-SEP-1997: 97KR-0047147.

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17-SEP-1987. 0748-0043117

PR 12-SEP-1997; 9/KK-0047147.

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PA (KOAD) KOREA ADV INST SCI &amp; TECHNOLOGY.

XX

PT Chung BH. Kim S.T. Lee SC. Kang HA. Choi HS.

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1000



CC of human cancers.  
SQ Sequence 46 BP; 12 A; 9 C; 15 G; 10 T; 0 other;  
Query Match 13.5%; Score 16.2; DB 17; Length 46;  
Best Local Similarity 60.0%; Pred. No. 3.4e+04;  
Matches 27; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 5 TGCATAGTGCCTCTACCCACACCTCATTTATCCCACTCCA 49  
||||| | | |||| | | | |||| | ||||| |  
Db 45 TGCATGTTTTCCTCTACCGACTCATCAGAGGCCCACTCGA 1  
RESULT 66  
ABK40901  
ID ABK40901 standard; DNA: 47 BP.  
AC ABK40901;  
XX  
XX  
XX  
XX 21-MAY-2002 (first entry)  
XX Human obesity-associated chromosome 10 biallelic marker #109.  
XX  
XX Human; obesity associated-biallelic marker; chromosome 10; obesity; ds;  
XX drug response; hyperuricaemia; digestive pathology; hypertension; cancer;  
XX hepatic function disorder; cardiovascular disease; hyperlipidaemia;  
XX insulin disorder; atheromatous disease; cardiac insufficiency.  
XX  
XX Homo sapiens.  
XX  
XX WO200206525-A2.  
XX  
XX 24-JAN-2002.  
XX  
XX 28-JUN-2001; 2001WO-IB01477.  
XX  
XX 18-JUL-2000; 2000US-219704P.  
XX  
XX (GEST ) GENSET.  
XX  
XX Cohen D; Blumenfeld M, Chumakov I, Abderrahim H, Bihain B;  
XX WPI; 2002-155043/20.  
XX  
XX Set of novel map-related biallelic markers, preferably located on  
XX obesity disorder-associated chromosomal regions on chromosomes 3, 10  
XX and 19, useful, for e.g. detecting statistical correlations between  
XX marker allele and a phenotype.  
XX  
XX Claim 1; Page 223; 31pp; English.  
XX  
XX The invention relates to a set of novel map-related biallelic markers,  
XX preferably located on obesity disorder-associated chromosomal regions on  
XX chromosomes 3, 10 and 19. The markers are useful for genotyping or  
XX estimating the frequency of an allele in a population, for detecting an  
XX association between a genotype or haplotype and a phenotype, e.g. a  
XX disease involving drug responses, obesity or disorders related to  
XX obesity, such as hyperuricaemia, digestive pathology, hepatic function  
XX disorders, cancer, cardiovascular disease, hypertension, hyperlipidaemia,  
XX insulin disorders, atheromatous disease and cardiac insufficiency. The  
XX markers are useful for detecting a statistical correlation between a  
XX biallelic marker allele and a phenotype and/or between a biallelic marker  
XX haplotype and a phenotype. This sequence represents a human  
XX obesity-associated biallelic marker located on chromosome 10.  
XX  
XX Sequence 47 BP; 11 A; 24 C; 2 G; 9 T; 1 other;  
Query Match 13.5%; Score 16.2; DB 24; Length 47;  
Best Local Similarity 64.9%; Pred. No. 3.4e+04;  
Matches 24; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 15 ACCCTCTAACCCACCTCATATATCCCACTCCAGA 51  
||||| ||||| ||| | ||||| |||

Db 3 ACCACCTTACCCAGTCTTCRCCTTCCACACCTCGA 39  
RESULT 67  
AAAS8433/C  
ID AAAS8433 standard; DNA: 48 BP.  
XX  
XX AAAS8433;  
XX  
XX 11-OCT-2000 (first entry)  
XX Human Factor VIIIC 67/70kd doublet probe #4.  
XX  
XX Factor VIII C domain; human; blood clotting; haemophilia; probe: ss.  
XX  
XX Homo sapiens.  
OS  
XX EP1006182-A2.  
XX  
XX 07-JUN-2000.  
XX  
XX 11-JAN-1985; 2000EP-0200860.  
XX  
XX 12-JAN-1984; 84US-0570062.  
XX 26-OCT-1984; 84US-0664919.  
XX 11-JAN-1985; 85EP-0100223.  
XX 11-JAN-1985; 91EP-0113267.  
XX  
XX (CHIR ) CHIRON CORP.  
XX (NOVO ) NOVO-NORDISK AS.  
XX  
XX Kuo G, Rasmussen ME, Masiarz FR, Valenzuela P, Truett M;  
XX Favaloro J;  
XX  
XX WPI; 2000-367967/32.  
XX  
XX DNA sequence of portion of human Factor VIIIC for treating and  
XX preventing the symptoms of haemophilia.  
XX  
XX Claim 10; Page 5; 39pp; English.  
XX  
XX The present sequence is a probe for the human Factor VIIIC 67/70kd  
XX doublet, which can be obtained by thrombin digestion of the 77/80kd  
XX fragments of the protein. The probe was created using the partial  
XX N-terminal sequence of the two fragments. Factor VIIIC is a plasma  
XX protein involved in blood coagulation, and is absent or defective in  
XX haemophilia A. The Factor VIIIC protein can, therefore, be used to  
XX treat haemophilia, as well as in the production of monoclonal antibodies  
XX to Factor VIIIC, and in diagnostic assays for the presence of Factor  
XX VIIIC subunits in physiological fluids, for example blood or serum.  
XX  
XX Sequence 48 BP; 9 A; 14 C; 8 G; 9 T; 8 other;  
Query Match 13.5%; Score 16.2; DB 21; Length 48;  
Best Local Similarity 46.7%; Pred. No. 3.4e+04;  
Matches 21; Conservative 8; Mismatches 16; Indels 0; Gaps 0;  
QY 2B ACACCTCATATCCCACTCCAGAGGATTCAGGGGTTCCAGCGT 72  
||||| | |||| | | | |||| | ||||| |  
Db 46 KCATYACTTATCCGTCGCTGGARAGCTGTGGGATYACGGCAT 2  
||||| | |||| | | | |||| | ||||| |  
RESULT 68  
AAQ88986/C  
ID AAQ88986 standard; RNA: 50 BP.  
XX  
XX AAQ88986;  
XX  
XX 28-SEP-1995 (first entry)  
XX VEGF 2'-NH2-RNA nucleic acid ligand family 1, oligo 28B.  
XX  
XX Nucleic acid; ligand; thrombin; elastase; theophylline; caffeine.  
XX



PF 22-JUN-1998: 98WO-US12930.  
 XX  
 PR 24-JUN-1997: 97US-0050594.  
 XX  
 PA (AFFY-) AFFYMETRIX INC.  
 XX  
 PI Berno A., Chee M., Fan J., Lipshutz RJ.  
 XX  
 DR WPI: 1999-080963/07.  
 XX  
 XX New nucleic acid segments containing polymorphic sites - used for,  
 XX e.g. detecting a disease phenotype, in forensics, paternity testing  
 PT or genetic mapping of phenotypic traits  
 XX  
 PS Claim 1: Page 33: 61pp: English.  
 XX  
 XX Sequences AA06101-X0558 represent human DNA fragments which contain  
 CC biallelic polymorphic markers. The base occupying the polymorphic site  
 CC is indicated by the appropriate IUPAC-IUB ambiguity code. These  
 CC fragments can be used in a method for determining polymorphic forms in  
 CC an individual. The invention further provides computer-readable storage  
 CC medium for storing data for access by an application programme being  
 CC executed on a data processing system. Such a method comprises a data  
 CC structure stored in the computer-readable storage medium, the data  
 CC structure including information resident in a database used by the  
 CC application programme and including records, each record comprising  
 CC information identifying a polymorphism shown in the above sequences. The  
 CC products and methods can be used for analysing polymorphic sites in  
 CC individuals for testing for the presence of a disease phenotype or in  
 CC forensics, paternity testing or genetic mapping of phenotypic traits.  
 CC They can also be used for the production of polypeptides expressed by  
 CC variant genes and for the production of transgenic animals. The nucleic  
 CC acid segments can also be used in the manufacture of medicaments for the  
 CC treatment or prophylaxis of diseases.  
 XX  
 XX Sequence 31 BP: 13 A; 3 C; 5 G; 9 T; 1 other:  
 SQ  
 Query Match 13.3% Score 16: DB 20: Length 31;  
 Best Local Similarity 73.1% Pred. No. 3.5e+04;  
 Matches 19: Conservative 1: Mismatches 6: Indels 0: Gaps 0;  
 QY 64 TTCAGCGTTCCTGAAATGATCGAT 89  
 DB 26 TTCCACATTCCTGTAATATGGAT 1  
 RESULT 71  
 AAF57140  
 ID AAF57140 standard; DNA: 42 BP.  
 XX  
 AC AAF57140;  
 XX  
 XX 29-MAY-2001 (first entry)  
 XX  
 DE OmpA-8L-IL-2 gene fusion generating primer.  
 XX  
 XX AGB; therapeutic: prophylactic; attenuated gram-negative bacterium;  
 KW bacteriophage; capsid protein; tumour; cancer; melanoma; fusogenic;  
 KW cytostatic; gene therapy; OmpA; PCR primer; Interleukin; IL2; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200114579-A2.  
 XX  
 PD 01-MAR-2001.  
 XX  
 PF 24-AUG-2000: 2000WO-US23243.  
 XX  
 PR 26-AUG-1999: 99US-0150928.  
 XX  
 PA (VION-) VION PHARM INC.  
 XX  
 PI Bermudes DG, King IC, Clairmont CA;

XX WPI: 2001-218457/22.  
 XX  
 PT Delivering a therapeutic agent to a subject for treating tumors, by  
 PT administering an attenuated bacterial vector comprising a bacteriophage  
 PT encoding a gene of interest  
 XX  
 PS Example: Page 45: 63pp: English.  
 XX  
 XX The invention relates to delivery of an agent which can be therapeutic or  
 CC prophylactic. The method involves administering a composition comprising  
 CC an attenuated gram-negative bacterium (AGB) containing a bacteriophage  
 CC genome which has been modified to encode for a gene product of interest  
 CC under control of a eukaryotic promoter or as a fusion protein with a  
 CC bacteriophage capsid protein. The method is useful for delivering an  
 CC agent to a subject, for inhibiting solid tumour growth or reducing an  
 CC tumour volume, in breast, prostate, cervical, uterine, lung, ovarian,  
 CC testicular, thyroid, renal, bladder, pancreatic, stomach, liver or colon  
 CC cancers and in astrocytoma, glioma, mesothelioma, and melanoma. The  
 CC present sequence represents a primer used for generating a OmpA-8L-  
 CC Interleukin (IL)-2 gene fusion.  
 XX  
 SQ Sequence 42 BP: 11 A; 7 C; 10 G; 14 T; 0 other:  
 Query Match 13.3% Score 16: DB 22: Length 42;  
 Best Local Similarity 62.5% Pred. No. 3.9e+04;  
 Matches 25: Conservative 0: Mismatches 15: Indels 0: Gaps 0;  
 QY 53 GGATTCAGGGGTTCCAGCGTTCCTGAAATGATCGATGG 92  
 DB 3 GAATTCGATATCTTCAGTTAAACGCTGAATGATCGATGG 42  
 RESULT 72  
 AAV56632/c  
 ID AAV56632 standard; DNA: 44 BP.  
 XX  
 AC AAV56632;  
 XX  
 DT 23-NOV-1998 (first entry)  
 XX  
 DE Feline FLAP cDNA primer #3.  
 XX  
 KW Cytokine; feline; FLAP#40; FLAP#5; heterodimer; cytotoxic; treatment;  
 KW T lymphocyte cell; autoimmune disease; primer; ss.  
 XX  
 OS Synthetic.  
 OS Fells catus.  
 XX  
 PN WO9746583-A1.  
 XX  
 PD 11-DEC-1997.  
 XX  
 PF 29-MAY-1997: 97WO-JP01824.  
 XX  
 PR 04-JUN-1996: 96JP-0165249.  
 XX  
 PA (KAGA ) CEMO-SERO-THERAPEUTIC RES INST.  
 XX  
 PI Fujiyasu T, Imagawa Y, Imamura T, Maeda H, Tokiyoshi S;  
 XX  
 DR WPI: 1998-042118/04.  
 XX  
 PT Novel feline cytokine protein - useful for treating feline  
 PT autoimmune diseases, e.g. those caused by feline herpes virus or  
 PT feline calicivirus  
 XX  
 PS Example 5: Page 61: 94pp: Japanese.  
 XX  
 XX AAV56630-V56636 are primers used in the amplification of novel feline  
 CC cytokine proteins, FLAP#40 and FLAP#5. This protein can be used in the  
 CC production of a FLAP#35/FLAP#40 heterodimer which can potentiate the  
 CC cytotoxic activity of feline cytotoxic T lymphocyte cells. Such proteins

CC are used for treatment of feline autoimmune diseases e.g. as caused by  
 CC feline herpes virus or feline calicivirus.

SQ Sequence 44 BP; 16 A; 7 C; 11 G; 10 T; 0 other:

Query Match 13.3%; Score 16; DB 19; Length 44;  
 Best Local Similarity 62.5%; Pred. No. 3.9e+04;  
 Matches 25; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 32 CTCTATATCCCATCCAGAGGATTCAGGCTTCACGC 71  
 II II IIIII I I I IIIII I III I I  
 DB 41 CTTATATCCCTGTGTGCGACCAATTCAGCTTTCTAGAG 2

## RESULT 73

AAL29218/C  
 ID AAL29218 standard; DNA: 45 BP.

XX  
 AC AAN90164;

XX 01-NOV-1989 (first entry)

XX Probe 643, hybridising to Salmonella rRNA.

XX Probe 643; Salmonella; rRNA; pattern 1; assay.

XX W08905359-A.

XX 15-JUN-1989.

XX 30-NOV-1988; 88MO-US04266.

XX 01-DEC-1987; 87US-0127484.

XX (INTE ) INTEGRATED GENETICS INC.

XX Lane DJ, Rashtchian A, Paroxos K;

XX WPI: 1989-192705/26.

XX Detection of Salmonella - using nucleic acid fragment capable of  
 PT hybridising to Salmonella RNA and not to that of Escherichia coli.

XX Disclosure; fig 5-2; 55pp; English.

XX Probe 643 hybridises to rRNA of Salmonella, but not to E.coli  
 CC or other Enterobacter strains. Used to detect Salmonella in food and  
 CC clinical samples. rRNA is abundant in cells and appears not to be  
 CC laterally transferred between contemporary organisms.

XX Sequence 45 BP; 11 A; 17 C; 5 G; 12 T; 0 other:

Query Match 13.3%; Score 16; DB 10; Length 45;  
 Best Local Similarity 62.5%; Pred. No. 4e+04;  
 Matches 25; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 66 CCAGGCTTCCTGAAATGATTCAGTTCCTTCATGCTGC 105  
 II IIIII I I I IIIII I IIIII I  
 DB 3 CCTCTCTCCACACACCAATTTATGCGCTGTTAACTGC 42

## RESULT 74

AAL29218/C  
 ID AAL29218 standard; DNA: 50 BP.

XX  
 AC AAL29218;

XX 24-JAN-2002 (first entry)

XX Human SNP oligonucleotide #2426.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;

KW anyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.

XX Homo sapiens.

XX W0200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000MO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI: 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections.

XX Claim 1: Page 2077; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic  
 CC variants of proteins related to amylases, anyloid proteins, angiotensin,  
 CC apoptosis related proteins, adhering cyclin, polymerase, platelets,  
 CC histones, kinases, colony stimulating factors, complement, interleukins,  
 CC G-protein coupled receptors, cytochromes, cytokines, interferon, interleukins,  
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
 CC by them may be used in the prevention, diagnosis and treatment of  
 CC diseases associated with inappropriate expression of the proteins listed  
 CC above. Disorders that may be prevented, diagnosed and/or treated include  
 CC multifactorial diseases with a genetic component, such as autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukaemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms.

XX Sequence 50 BP; 9 A; 11 C; 15 G; 15 T; 0 other:

Query Match 13.3%; Score 16; DB 22; Length 50;  
 Best Local Similarity 62.5%; Pred. No. 4.1e+04;

Matches 25; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 43 CACTCCAGAGGATTCAGGCTTCAGGCTTCCTGAAAT 82  
 I IIIII I I I IIIII IIIII I I I  
 DB 50 CCCCCCAGAGAGACCCAAAGGTCAGTGTCTTGCGAT 11

## RESULT 75

AAL31258

ID AAL31258 standard; DNA: 50 BP.

XX

AC AAL31258;

XX 24-JAN-2002 (first entry)

XX Human SNP oligonucleotide #4466.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KW anyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;

KW Interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200147944-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 28-DEC-2000; 2000WO-US35498.  
XX  
PR 28-DEC-1999; 99US-0173419.  
XX  
PR 27-DEC-2000; 2000US-0173419.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkets RA, Leach M;  
XX  
DR WPI: 2001-465210/50.  
XX  
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g.  
PT cancer, autoimmune diseases and infections -  
XX  
PS Claim 1; Page 2670; 4143pp; English.  
XX  
CC The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.  
XX  
SQ Sequence 50 BP; 9 A; 19 C; 16 G; 6 T; 0 other;  
Query Match 13.3% Score 16; DB 22; Length 50;  
Best Local Similarity 68.8%; Pred. No. 4.1e+04;  
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
OY 39 TCCCACTCCAGAGGATTCAGGGGTCACGC 70  
DB 8 TCCCACTCCAGAGGATTCAGGGGTCACGC 39  
RESULT 76  
ID AAL32049 standard; DNA: 50 BP.  
XX  
AC AAL32049;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Human SNP oligonucleotide #5257.  
XX  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.

XX  
OS Homo sapiens.  
XX  
PN WO200147944-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 28-DEC-2000; 2000WO-US35498.  
XX  
PR 28-DEC-1999; 99US-0173419.  
XX  
PR 27-DEC-2000; 2000US-0173419.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkets RA, Leach M;  
XX  
DR WPI: 2001-465210/50.  
XX  
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g.  
PT cancer, autoimmune diseases and infections -  
XX  
PS Claim 1; Page 2900; 4143pp; English.  
XX  
CC The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of pathogenic  
CC organisms.  
XX  
SQ Sequence 50 BP; 14 A; 9 C; 18 G; 9 T; 0 other;  
Query Match 13.3% Score 16; DB 22; Length 50;  
Best Local Similarity 68.8%; Pred. No. 4.1e+04;  
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
OY 77 GAAATGATTCAGGGGTCAGGGGTCAGGCTGCTCA 108  
DB 2 GAAATGATTCAGGGGTCAGGGGTCAGGCTGCTCA 33  
RESULT 77  
ID AAL78645/C  
XX  
AC AAL78645;  
XX  
DT 09-NOV-2001 (first entry)  
XX  
DE Human silent SNP containing nucleic acid SEQ:5586.  
XX  
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
KW protein therapy; vaccine; probe; diagnostic assay; detection;  
KW quantitation; restorative therapy; polymorphic; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200140521-A2.  
XX  
PD 07-JUN-2001.  
XX  
PF 30-NOV-2000; 2000WO-US32758.



```

XX 30-NOV-1999: 99US-0168138.
XX 29-NOV-2000: 2000US-0726173.
XX (CURA-) CURAGEN CORP.
XX Shimkels RA, Leach M.
XX WPI: 2001-356160/37.
XX Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy.
XX Claim 1: Page 2219; 263pp: English.
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
XX sequences (I), which contain single nucleotide polymorphisms (SNPs).
XX AA173114 to AA173329 represent peptides related to human polymorphic
XX polynucleotide sequences. The sequences can be used in gene and protein
XX therapy, and in vaccine production. (I) and the polypeptides encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate expression of polymorphic polypeptides.
XX For example, (I) may be used to treat disorders by rectifying mutations
XX or deletions in a patient's genome that affect the activity of
XX polypeptides by expressing inactive proteins or to supplement the
XX patients own production of polypeptide. Additionally, (I) and its
XX complementary sequences may also be used as DNA probes in diagnostic
XX assays to detect and quantitate the presence of similar nucleic acids
XX in samples, and therefore which patients may be in need of restorative
XX therapy. The polypeptides encoded by (I) may be used as antigens in the
XX production of antibodies specific for polymorphic polypeptides. The
XX antibodies may also be used to down regulate expression and activity.
XX The antibodies may also be used as diagnostic agents for detecting the
XX presence of polymorphic polypeptides in samples.
XX Sequence 50 BP; 9 A; 12 C; 16 G; 13 T; 0 other:
XX
XX Query Match 13.34; Score 16; DB 22; Length 50;
XX Best Local Similarity 62.54; Pred. No. 4.1e+04;
XX Matches 25; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
XX
XX 8 CATAGTACCTCTACACACACCTCTATTATCCGACTG 47
XX 11111111111111111111111111111111
XX 43 CAGACGACGGCGATGTGCCACATGACATTCACACCATC 4
XX
XX RESULT 78
XX AAN92541
XX ID AAN92541 standard; DNA: 27 BP.
XX AC AAN92541;
XX DT 03-OCT-2002 (updated)
XX DT 20-JUN-1990 (first entry)
XX XX
XX Tag sequence of a multiplex vector.
XX
XX Multiplex sequencing: DNA sequencing; Maxam-Gilbert; Sanger; ss.
XX Synthetic.
XX PN EP303459-A.
XX PD 15-FEB-1989.
XX PF 10-AUG-1988: 88EP-0307391.
XX PR 11-AUG-1987: 87US-0084623.
XX PA (HARD) HARVARD COLLEGE.
XX PI Church GM, Kieffer-Higgins S;
XX

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```

XX WPI: 1989-048232/07.
XX Rapid DNA sequencing.
XX PT using multiplex vectors provided with a DNA sequence having a
XX PT cloning site, at least one tag sequence with opt. removable sites.
XX
XX Example 2: Fig 3: 16pp: English.
XX
XX Tag is applied to DNA to be sequenced and after random fragmentation, DNA
XX will have tag sequence on one end and identifiable (Maxam and Gilbert or
XX Sanger) bases at the other, allowing sequencing. The significantly
XX increases the speed at which the sequencing can be performed.
XX (Updated on 03-OCT-2002 to add missing OS field.)
XX
XX Sequence 27 BP; 8 A; 12 C; 0 G; 7 T; 0 other:
XX
XX Query Match 13.24; Score 15.8; DB 10; Length 27;
XX Best Local Similarity 74.14; Pred. No. 3.9e+04;
XX Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
XX 16 CCTCTTAACCCACACCTCTATTATCCC 42
XX 11111111111111111111111111111111
XX 1 CCTTCTTAACCCACACCTCTATTATACC 27
XX
XX RESULT 79
XX AAX58157/C
XX ID AAX58157 standard; DNA: 31 BP.
XX AC AAX58157;
XX DT 21-JUL-1999 (first entry)
XX DE Primer catl(+) for Cdc-fusion protein construction.
XX
XX Cdc: fusion protein: erythropoietin receptor dimerisation domain;
XX Protein-protein interaction; periplasmic domain; transmembrane domain;
XX Cdc transcriptional regulatory domain; receptor interaction;
XX Ligand identification; orphan receptor; ss.
XX
XX Synthetic.
XX PN M09923116-A1.
XX PD 14-MAY-1999.
XX PF 03-NOV-1998: 98WO-US23307.
XX PR 09-SEP-1998: 98US-0145922.
XX PR 03-NOV-1997: 97US-0064058.
XX PA (SMAL-) SMALL MOLECULE THERAPEUTICS INC.
XX PI Hsing M, Menzel R, Taggart PA;
XX WPI: 1999-313305/26.
XX
XX New Cdc-fusion polypeptide nucleic acid constructs
XX
XX Example: Page 68: 123pp: English.
XX
XX This sequence represents a PCR primer used in the construction of a
XX Cdc-fusion polypeptide.
XX The invention relates to Cdc-fusion polypeptide nucleic acid constructs,
XX which are used to transform cells to produce systems for identifying
XX compounds which modulate interactions between protein sequences. The
XX Cdc-fusion polypeptides comprise a periplasmic domain, a transmembrane
XX domain and a Cdc transcriptional regulatory domain. Cells transformed
XX with nucleic acid encoding the fusion proteins and a cDNA reporter
XX construct can be used for identifying compounds which modulate a specific
XX protein-protein interaction such as modulation of interactions between
XX protein sequences involved in receptor interactions, e.g. dimerisation.
XX Such methods can be used for identifying ligands for orphan receptors.
XX

```

CC The system is extremely sensitive in that background is low and the  
 CC magnitude of signal background is quite robust, such that even minor  
 CC modulations in protein-protein interactions are readily detectable.

XX SQ Sequence 31 BP; 11 A; 6 C; 10 G; 4 T; 0 other;  
 Query Match 13.2%; Score 15.8; DB 20; Length 31;  
 Best Local Similarity 74.1%; Pred. No. 4.1e-04;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 89 TTGGCTTCATAGCTCTGTAATTCAG 115  
 DB 27 TTAGCTTCCTAGCTCTGATCCGG 1

## RESULT 80

AAC65624  
 ID AAC65624 standard; DNA; 31 BP.

XX AC AAC65624;

XX DT 16-FEB-2001 (first entry)

XX DE S. aureus OS2 srtA PCR primer orf6C-dt-B.

XX KW Sortase transamidase; Gram-positive bacterium; covalent cross-link;  
 KW peptidoglycan; antibacterial; vaccine; treatment; detection;  
 KW bacterial infection; primer: srtA; ss.

XX OS Staphylococcus aureus.

XX PN W0200062804-A2.

XX PD 26-OCT-2000.

XX PF 13-APR-2000; 2000WO-US10198.

XX PR 15-APR-1999; 99US-0292437.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Schneewind O, Mazmanian S, Liu G, Ton-That H;

XX DR WPI: 2000-665197/64.

XX A substantially purified sortase-transamidase from a Gram-positive  
 PT bacterium for use in the treatment and detection of Gram-positive  
 PT bacterial infections.

XX PS Example, 3; Page 61; 126pp; English.

XX CC This invention describes a novel substantially purified  
 CC sortase-transamidase (1) from a Gram-positive bacterium, catalyzing a  
 CC covalent cross-linking of the carboxyl terminus of a protein having a  
 CC sorting signal to the peptidoglycan of a Gram-positive bacterium, the  
 CC signal comprising a LPX<sub>3-4C</sub> motif where sorting involves cleavage  
 CC between the fourth and fifth residues of the motif. The products of  
 CC the invention have antibacterial activity and can be used in a vaccine.  
 CC The enzyme is useful in the treatment and detection of Gram-positive  
 CC bacterial infections, especially immunocompromized patients having  
 CC Mycobacterium infections. (1) is useful for screening for expression of a  
 CC cloned polypeptide. The transformed host cells are useful for the  
 CC production of substantially purified sortase-transamidase.

XX SQ Sequence 31 BP; 10 A; 6 C; 6 G; 9 T; 0 other;  
 Query Match 13.2%; Score 15.8; DB 21; Length 31;  
 Best Local Similarity 74.1%; Pred. No. 4.1e-04;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 79 AAATGATGATTGGCTTCATAGCTGC 105  
 DB 1 AAAGATCCCTTGACTCTGTAGCTAC 27

## RESULT 81

AAT36269/c  
 ID AAT36269 standard; DNA; 33 BP.

XX AC AAT36269;

XX DT 15-APR-1997 (first entry)

XX DE Probe CAT 03, binds to nucleotides 518-550.

XX KW Primer: PCR; amplify; polymerase chain reaction; murine leukaemia virus;  
 KW chloramphenicol acetyl transferase; CAT; pLXSn-cat; retroviral vector;  
 KW deoxyribonucleotide triphosphate; transduction efficiency; backbone; ss.

XX OS Synthetic.

XX PN W09624677-A1.

XX PD 15-AUG-1996.

XX PF 08-FEB-1996; 96WO-US01958.

XX PR 08-FEB-1995; 95US-0385446.

XX PA (UVJE-) UNIV JEFFERSON THOMAS.

XX PI Pomerantz RJ, Zhang H;

XX DR WPI: 1996-384449/38.

XX Increasing transduction efficiency of retroviral vectors - by  
 PT pre-incubation with deoxy-nucleotide triphosphate(s), for use in  
 PT gene therapy or protein prodn.

XX PS Disclosure: Page 6; 22pp; English.

XX CC This sequence represents a P32 labelled probe which was used in the  
 CC isolation of the chloramphenicol acetyl transferase (CAT) gene.  
 CC The isolated sequence was cloned into a plasmid, e.g. pLXSn-cat  
 CC containing the CAT gene in a murine leukaemia virus backbone, and  
 CC used to test the method of the invention. The method comprises  
 CC incubating retroviral vectors with deoxyribonucleotide triphosphates  
 CC before transduction to improve transduction efficiency. Incubation  
 CC with deoxyribonucleotide triphosphates allows the vector to complete  
 CC reverse transcription of the RNA genome, producing double-stranded  
 CC heteroduplex viruses which have higher infectivity, and are therefore  
 CC more effective vectors. The need for virion envelope permeabilisation  
 CC and preparation of very high titre virus stock is eliminated.

XX SQ Sequence 33 BP; 9 A; 7 C; 7 G; 10 T; 0 other;

Query Match 13.2%; Score 15.8; DB 17; Length 33;  
 Best Local Similarity 74.1%; Pred. No. 4.2e-04;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 43 CACTCCAGAGGATTCAGGGTTCCAG 69  
 DB 28 CACTCCAGAGCGATGAACGTTTCAG 2

## RESULT 82

AAV51211/c  
 ID AAV51211 standard; DNA; 41 BP.

XX AC AAV51211;

XX DT 11-JAN-1999 (first entry)

XX DE Maize polymorphic marker S10G4/G6-1 DNA.

XX KW Polymorphic marker: allele-specific; primer; probe; amplification;



CC mucosa and the repair of acute and chronic mucosal lesions (e.g.  
 CC enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration  
 CC and congenital microvillus atrophy), skin diseases associated with  
 CC abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers  
 CC such as lung squamous cell carcinoma of the vulva and gliomas), potent  
 CC effects on cell growth and development, diseases related to growth or  
 CC survival of nerve cells including Parkinson's disease, Alzheimer's  
 CC disease, ALS, neuropathies or cancer. PRO285 can be used as for  
 CC fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a  
 CC target for anti-tumor drugs. PRO533 may be used in the treatment of Usher  
 CC Syndrome or Atrophia areas. PRO269 can be used as an anti-thrombotic  
 CC agent; PRO287 polypeptides and portions may have therapeutic applications  
 CC in wound healing and tissue repair; PRO317 can be used for treating  
 CC problems of the kidney, uterus, endometrium, blood vessels, or related  
 CC tissues, e.g. in the heart of genital tract.  
 XX  
 SQ Sequence 45 BP; 8 A; 11 C; 15 G; 11 T; 0 Other;

Query Match 13.28; Score 15.8; DB 20; Length 45;  
 Best Local Similarity 74.18; Pred. No. 4.7e+04;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 29 CACCTCATTATCCCTCCAGAGGGA 55  
 DB 28 CCCACATACCTCCACAGCCGAGGGA 2

## RESULT 84

AA772638/C  
 ID AA772638 standard; DNA: 45 BP.

XX  
 AC AA772638:

DT 24-APR-2001 (first entry)

DE Human PRO polypeptide gene oligonucleotide OLI2692.

XX Human: PRO: dermatological; antipsoriatic; cytostatic; antiinflammatory;  
 KW antiparkinsonian nootropic; neuroprotective; vulvar; cardiant;  
 KW antiangiogenic; vasotropic; antisthmatic; antirheumatic; cancer;  
 KW antiarthritic; antinfertility; antidiabetic; antihypertensive;  
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;  
 KW ischaemia; inflammation; PCR primer; probe; ss.

XX Homo sapiens.

XX WO200104311-A1.

XX 18-JAN-2001.

XX 22-FEB-2000; 2000WO-US04414.

XX 07-JUL-1999; 99US-0143048.

XX 26-JUL-1999; 99US-0145698.

XX 28-JUL-1999; 99US-0146222.

XX 08-SEP-1999; 99WO-US20594.

XX 13-SEP-1999; 99WO-US20944.

XX 15-SEP-1999; 99WO-US21090.

XX 15-SEP-1999; 99WO-US21547.

XX 05-OCT-1999; 99WO-US23089.

XX 29-NOV-1999; 99WO-US28214.

XX 30-NOV-1999; 99WO-US28313.

XX 16-DEC-1999; 99WO-US30095.

XX 20-DEC-1999; 99WO-US30999.

XX 05-JAN-2000; 99WO-US00219.

XX (GETH) GENEMTECH INC.

XX Ashkenazi AJ, Botstein D, Desnovers L, Eaton DL, Ferrara N,

PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;

PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;

PI Williams PM, Wood WI;

XX WPI; 2001-081051/09.

DR Sixty one nucleic acids encoding PRO polypeptides which are useful in  
 XX the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung  
 PT squamous cell carcinoma) and neurodegenerative diseases (e.g.  
 PT Alzheimer's disease).

XX Example 46: page 192; 393pp; English.

XX The present sequence is an oligonucleotide used in the isolation of one  
 CC of sixty one nucleic acids encoding novel secreted and transmembrane PRO  
 CC polypeptides. The PRO polypeptides are useful for treating skin diseases  
 CC (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma)  
 CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative  
 CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,  
 CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,  
 CC ischaemia such as coronary ischaemia, atherosclerosis), inflammatory  
 CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),  
 CC infertility, AIDS and diabetes and retinal disorders such as retinitis  
 CC pigmentosum. The PRO nucleic acids have applications in molecular  
 CC biology, including use as hybridization probes, and in chromosome and  
 CC gene mapping.

XX Sequence 45 BP; 8 A; 11 C; 15 G; 11 T; 0 other;

Query Match 13.28; Score 15.8; DB 22; Length 45;

Best Local Similarity 74.18; Pred. No. 4.7e+04;

Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 29 CACCTCATTATCCCTCCAGAGGGA 55

DB 28 CCCACATACCTCCACAGCCGAGGGA 2

## RESULT 85

ABK28585/C

ID ABK28585 standard; DNA: 45 BP.

XX AC ABK28585;

XX 09-APR-2002 (first entry)

XX Human PRO346 hybridisation probe OLI2692.

XX Human: ss: PRO: antiinflammatory; ophthalmological; vasotropic;  
 KW retinal cell injury; ocular disease; retinitis pigmentosa; probe;  
 KW macular degeneration; retinal detachment; retinal tear; retinopathy;  
 KW retinal degenerative disease; macular hole; degenerative myopia;  
 KW acute retinal necrosis syndrome; traumatic chorioretinopathy;  
 KW Purtscher's retinopathy; oedema; ischaemic condition;  
 KW retinal vision occlusion; collagen vascular disease;  
 KW thrombocytopaenic purpura; uveitis; retinal vasculitis; Eales disease;  
 KW systemic lupus erythematosus; environmental trauma.

XX Homo sapiens.

XX WO200109327-A2.

XX 08-FEB-2001.

XX 28-JUL-2000; 2000WO-US20710.

XX 28-JUL-1999; 99US-146222P.

XX 13-SEP-1999; 99WO-US20944.

XX 15-SEP-1999; 99WO-US21090.

XX 29-NOV-1999; 99WO-US28214.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1999; 99WO-US28301.

XX 05-JAN-2000; 2000WO-US00219.

XX 06-JAN-2000; 2000WO-US00376.

XX 11-FEB-2000; 2000WO-US03565.



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XX Key Location/Qualifiers
FH Variation replace(24,T)
FT /tag- a
FT /standard_name- "single nucleotide polymorphism"
XX
XX W09954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99MO-1B0C822.
XX
XX 21-APR-1998; 98US-0082614.
XX
XX 23-NOV-1998; 98US-0109732.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI: 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome
XX
XX Claim 3; Page 724; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the
XX invention have a variety of uses: they can be used for high density
XX mapping of the human genome, and in complex association studies and
XX haplotyping studies which are useful in determining the genetic basis
XX for disease states. Compositions and methods of the invention can also
XX be useful for the identification of the targets for the development of
XX pharmaceutical agents and diagnostic methods, as well as the
XX characterisation of the differential efficacious responses to and side
XX effects from pharmaceutical agents acting on a disease as well as other
XX treatment.
XX
XX N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
XX and 3367, are not actually given a sequence in the Sequence Listing
XX from the present invention.
XX
XX Sequence 47 BP; 10 A; 18 C; 7 G; 12 T; 0 other;
XX
Query Match 13.2%; Score 15.8; DB 21; Length 47;
Best Local Similarity 74.1%; Pred. No. 4.8e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 52 GGGATTCCAGGGTTCACGGTTCCTGA 78
DB 30 GGGTCCAGGGTTCACGAGATGCTGA 4
XX
RESULT 88
AAZ68911/C
ID AAZ68911 standard; DNA: 47 BP.
XX
XX AAZ68911;
XX
XX 10-SEP-2001 (first entry)
XX
XX Human map-related biallelic marker SEQ ID NO:3265.
XX
XX Human genome; biallelic marker; high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX diagnosis; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Variation replace(24,C)
FT

```

```

FT
XX /tag- a
XX /standard_name- "single nucleotide polymorphism"
XX
XX W09954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99MO-1B0C822.
XX
XX 21-APR-1998; 98US-0082614.
XX
XX 23-NOV-1998; 98US-0109732.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI: 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
XX map of the human genome
XX
XX Claim 3; Page 927; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX primers for the biallelic markers. The biallelic markers of the
XX invention have a variety of uses: they can be used for high density
XX mapping of the human genome, and in complex association studies and
XX haplotyping studies which are useful in determining the genetic basis
XX for disease states. Compositions and methods of the invention can also
XX be useful for the identification of the targets for the development of
XX pharmaceutical agents and diagnostic methods, as well as the
XX characterisation of the differential efficacious responses to and side
XX effects from pharmaceutical agents acting on a disease as well as other
XX treatment.
XX
XX N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
XX and 3367, are not actually given a sequence in the Sequence Listing
XX from the present invention.
XX
XX Sequence 47 BP; 14 A; 8 C; 18 G; 7 T; 0 other;
XX
Query Match 13.2%; Score 15.8; DB 21; Length 47;
Best Local Similarity 65.1%; Pred. No. 4.8e+04;
Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 23 AACCCACACCTCATTTATCCCACTCCAGAGGGATT 57
DB 46 AACCCAGGCTCTCTGATTCACACACCTGTCTT 12
XX
RESULT 89
AAH50322
ID AAH50322 standard; DNA: 47 BP.
XX
XX AAH50322;
XX
XX 22-AUG-2001 (first entry)
XX
XX Bacterial 23S/5S RNA detecting primer SEQ ID 517.
XX
XX Detection; spacer: 23S rDNA; 5S rDNA; probe; primer; phylogenetic group;
XX enterobacterium; clinical diagnosis; food contamination; ss.
XX
XX Streptomyces ambifaciens.
XX
XX DE19945916-A1.
XX
XX 05-APR-2001.
XX
XX 24-SEP-1999; 99DE-1045916.
XX
XX 24-SEP-1999; 99DE-1045916.
XX

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XX (BIOT-) BIOTECON DIAGNOSTICS GMBH.  
 XX Grabowski R, Berghof K;  
 XX WPI: 2001-246133/26.  
 XX New nucleic acid primers and probes, useful for bacterial detection, in  
 XX clinical diagnosis and detecting food contamination, comprises 23S and  
 XX 5S rDNA sequences  
 XX Claim 22: Page 122: 140pp: German.  
 XX This invention describes a novel nucleic acid molecule (I), useful as a  
 XX probe and/or primer for detecting bacteria. The invention also describes  
 XX (1) a combination of at least two nucleic acids (II) for detecting  
 XX bacteria or phylogenetic groups of bacteria, particularly enterobacteria;  
 XX (2) a kit containing (I) or the combination of (II); (3) detecting  
 XX bacteria (particularly enterobacteria) in a sample by contacting the  
 XX sample with (I) or the combination of (II) and detecting hybridization;  
 XX and (4) amplifying (M1) bacterial DNA from many different taxonomic  
 XX groups using (I) or the combination of (II) as primers. The method is  
 XX used to detect and identify bacteria, for clinical diagnosis and for  
 XX detecting contamination of food. (I) can detect bacteria at various  
 XX levels of selectivity (e.g., all bacteria, particular classes, families,  
 XX genera or species). The method exploits the fact that the 23S and 5S rDNA  
 XX regions, and the intermediate transcribed spacer, contain some sequences  
 XX that are highly conserved and others that are highly variable.  
 XX AAH9807-AAH50411 represent primers used to illustrate the method of the  
 XX invention.

XX Sequence 47 BP: 9 A: 9 C: 15 G: 14 T: 0 Other:

XX Query Match 13 28: Score 15.8: DB 22: Length 47:  
 XX Best Local Similarity 65.7%: Pred. No. 4.9e-04:  
 XX Matches 23: Conservative 0: Mismatches 12: Indels 0: Gaps 0:

QY 46 TCCAGGAGGATTTCAGGGTTCACGGCTCTCGAA 80  
 DB 6 TTCATAGTGTTCGGTGGTCATAGCGTTAGGAA 40

RESULT 90

AAH25966/c

ID AAH25966 standard: DNA: 50 BP.

XX AC AAH25966:

XX 11-SEP-2001 (first entry)

XX Rice genomic fragment B7-specific PCR primer B7F50, SEQ ID NO:44.

XX Rice: variety identification: characterisation: differentiation:  
 XX band pattern: RAPD fragment: random amplification of polymorphic DNA:  
 XX amplification: single grain sample: PCR primer: ss.

XX Oryza sativa.

XX JP2001095589-A.

XX 10-APR-2001.

XX 27-JUL-2000: 2000JP-0226854.

XX 27-JUL-1999: 99JP-0211915.

XX (NORR) NORINSUISANSHO SHOKUIN 5000.

XX (OTSU) OTSUBO K.

XX (YOGU) YOGURA K.

XX (KAWA) KAWASAKI S.

XX WPI: 2001-360497/38.

PT Differentiation of varieties of rice.  
 PS Disclosure: Page 20: 25pp: Japanese.  
 XX The invention relates to a PCR-based method of differentiating  
 XX between different varieties of rice. In particular, a single grain of  
 XX polished or cooked rice is used in the method. When rice DNA is  
 XX subjected to techniques such as RAPD (random amplification of  
 XX polymorphic DNA), different varieties of rice produce different  
 XX characteristic patterns of variously sized fragments (detected as bands  
 XX on an electrophoresis gel). The method of the invention uses sets of PCR  
 XX primers specific for the 5' and 3' ends of fragments designated S13,  
 XX M2CC, M11, R1, WKA9, J6, B16, M2F, T8, F6, Q16, B7 and A7 to amplify  
 XX rice genomic DNA. The amplified fragments are visualised via gel  
 XX electrophoresis. The presence or absence of particular amplified  
 XX fragments in a sample (the banding pattern) enables one variety of  
 XX rice to be distinguished from another. The method of the invention is  
 XX rapid, accurate, inexpensive and easily operable. Sequences  
 XX AAH25924-AAH25973 represent fragment-specific PCR primers used in the  
 XX method of the invention.

XX Sequence 50 BP: 10 A: 12 C: 17 G: 11 T: 0 Other:

XX Query Match 13 28: Score 15.8: DB 22: Length 50:

XX Best Local Similarity 74.1%: Pred. No. 4.9e-04:

XX Matches 20: Conservative 0: Mismatches 7: Indels 0: Gaps 0:

QY 7 CCATAGTACCCCTCTTACCCACACT 33

DB 28 CAAGCGTCATCTCTGTACCCACACT 2

RESULT 91

AAH89777

ID AAH89777 standard: DNA: 27 BP.

XX AC AAH89777:

XX 20-MAR-1998 (first entry)

XX Plasmid pET-E2.123 PCR primer EA21.

XX Human immunodeficiency virus: HIV Type 1; Tat protein; plasmid:  
 XX cargo molecules: intracellular delivery; fusion protein;  
 XX therapeutic; prophylactic; diagnostic; transport polypeptide;  
 XX human papillomavirus: E2 repressor protein; PCR primer: ss.

XX Synthetic.

XX Chimeric - Human Papillomavirus 16.

XX Chimeric - Bovine Papillomavirus Type 1

XX Chimeric - Human Immunodeficiency Virus Type 1.

XX US5674980-A.

XX 07-OCT-1997.

XX 21-DEC-1989: 89US-0454450.

XX 28-APR-1994: 94US-0235403.

XX 21-DEC-1989: 89US-0454450.

XX 02-JAN-1991: 91US-0636662.

XX 21-AUG-1992: 92US-0934375.

XX 19-AUG-1993: 93WO-0507833.

XX 24-NOV-1993: 93US-0158015.

XX 25-MAY-1995: 95US-0450098.

XX (BAKS) BARSOU J G.

XX (FAME) FAMELL S E.

XX (FRAN) FRANKEL A.

XX (PABO) PABO.

XX (PEPI) PEPINSKY R B.

XX Barsoum JG, Fawell SE, Frankel A, Pabo C, Pepinsky RB.

XX WPI: 1997-502388/46.  
 XX Fusion proteins containing truncated HIV tat sequences - useful for  
 PT intracellular delivery of viral repressor proteins  
 XX  
 XX Example 13: Column 93: 77pp: English.  
 XX This PCR primer is used with EA22 (AAT89778) to amplify a fragment of  
 CC the E2 repressor protein using the plasmid pCO-E2 as a template. This  
 CC fragment was ligated into NcoI-BamHI cleaved pET8c. Primer EA21  
 CC introduced an NcoI site that added a methionine codon followed by an  
 CC alanine (codon 5') adjacent to the coding region for the carboxy terminal  
 CC 101 residues of BPV-1 E2. The plasmids used in this study can be used in  
 CC a novel method for the delivery of biologically active cargo molecules  
 CC into the cytoplasm and nuclei of eukaryotic cells. The tat protein from  
 CC immunodeficiency virus (e.g. HIV-1, HIV-2, SIV) is readily taken up into  
 CC cells when present extracellularly and can be modified to covalently  
 CC link to cargo proteins e.g. the E2 repressor protein, producing a fusion  
 CC protein without the problems of spurious trans-activation and disulphide  
 CC aggregation. These transport polypeptides also minimise interference  
 CC with the biological activity of the cargo molecule. This is applicable  
 CC for therapeutic, prophylactic or diagnostic intracellular delivery of  
 CC small molecules and macromolecules e.g. proteins, nucleic acids and  
 CC polysaccharides.  
 XX  
 SQ Sequence 27 BP: 8 A: 8 C: 7 G: 4 T: 0 other:  
 Query Match 13.0% Score 15.6; DB 18: Length 27;  
 Best Local Similarity 81.8%; Pred. No. 4.6e+04;  
 Matches 18: Conservative 0; Mismatches 4; Indels 0; Gaps 0.  
 QY 3 GATGCCATAGTGACCCCTCCTAA 24  
 II IIIII IIIII IIIII II  
 Db 6 GAAGCCATGGTGACTCTCCCA 27  
 II IIIII IIIII IIIII II  
 RESULT 92  
 AAT8237  
 ID AAT8237 standard; DNA: 27 BP.  
 XX  
 AC AAT8237;  
 XX  
 DT 19-JAN-1998 (first entry)  
 XX  
 DE Primer EA21 for BPV-1 E2 repressor fragment.  
 XX  
 KW Chemical conjugate; transport polypeptide; tat protein; primer;  
 KW delivery; cytoplasm; cell nucleus; therapy; BPV-1; E2 repressor;  
 KW prophylaxis; diagnosis; spurious transactivation; HIV-1; PCR;  
 KW disulphide aggregation; human immunodeficiency virus type 1; ss.  
 XX  
 OS Synthetic.  
 OS Bovine papilloma virus 1.  
 XX  
 PN US5670617-A.  
 XX  
 PD 23-SEP-1997.  
 XX  
 XX 21-DEC-1989; 89US-0454450.  
 XX  
 PR 28-APR-1994; 94US-0235403.  
 PR 21-DEC-1989; 89US-0454450.  
 PR 02-JAN-1991; 91US-0636662.  
 PR 21-AUG-1992; 92US-0934375.  
 PR 19-AUG-1993; 93WO-US07833.  
 PR 24-NOV-1993; 93US-0158015.  
 PR 25-MAY-1995; 95US-0450246.  
 XX  
 XX (BARS/) BARSOUM J G.  
 PA (FAWE/) FAWELL S E.  
 PA (FRAN/) FRANKEL A.  
 PA (PABO/) PABO C.  
 PA (PEPI/) PEPINSKY R B.

PA (PEPI/) PEPINSKY R B.  
 PI Barsoum JG, Fawell SE, Frankel A, Pabo C, Pepinsky RB;  
 XX WPI: 1997-479523/44.  
 XX Conjugate for intracellular delivery - comprising transport moiety  
 PT having amino acids 49-57 of human immunodeficiency virus tat protein  
 PT and nucleic acid cargo moiety  
 XX  
 XX Example 13: Columns 93-94: 77pp: English.  
 XX The present sequence is a primer used in the preparation of  
 CC covalently linked chemical conjugate, comprising a transport  
 CC polypeptide moiety consisting of at least residues 49-57 of human  
 CC immunodeficiency virus (HIV) tat protein, but not residues 22-36  
 CC and 73-86, and a cargo moiety comprising bovine papilloma virus 1  
 CC (BPV-1) E2 repressor. Such conjugates can be used to deliver cargo  
 CC moieties into the cytoplasm and nuclei of cells for therapeutic,  
 CC prophylactic and diagnostic applications. The HIV tat protein is  
 CC readily taken up into cells and the cell nucleus. The reduced size  
 CC of the transport polypeptides minimises interference with the  
 CC biological activity of the cargo molecule. In addition, by virtue  
 CC of the absence of the cysteine rich region of the HIV tat protein,  
 CC the transport polypeptides solve the potential problems of  
 CC spurious transactivation and disulphide aggregation.  
 XX  
 SQ Sequence 27 BP: 8 A: 8 C: 7 G: 4 T: 0 other:  
 Query Match 13.0% Score 15.6; DB 18: Length 27;  
 Best Local Similarity 81.8%; Pred. No. 4.6e+04;  
 Matches 18: Conservative 0; Mismatches 4; Indels 0; Gaps 0.  
 QY 3 GATGCCATAGTGACCCCTCCTAA 24  
 II IIIII IIIII IIIII II  
 Db 6 GAAGCCATGGTGACTCTCCCA 27  
 II IIIII IIIII IIIII II  
 RESULT 93  
 AAT84579  
 ID AAT84579 standard; DNA: 27 BP.  
 XX  
 AC AAT84579;  
 XX  
 DT 16-DEC-1997 (first entry)  
 XX  
 DE Tat-E2 conjugate PCR primer EA21.  
 XX  
 KW HIV; tat protein; transport protein; cargo delivery; E2 repressor;  
 KW human immunodeficiency virus type 1; bovine papillomavirus; PCR;  
 KW primer; polymerase chain reaction; ss.  
 XX  
 OS Synthetic.  
 OS US5652122-A.  
 XX  
 PD 29-JUL-1997.  
 XX  
 XX 21-DEC-1989; 89US-0454450.  
 XX  
 PR 28-APR-1994; 94US-0235403.  
 PR 21-DEC-1989; 89US-0454450.  
 PR 02-JAN-1991; 91US-0636662.  
 PR 21-AUG-1992; 92US-0934375.  
 PR 19-AUG-1993; 93WO-US07833.  
 PR 24-NOV-1993; 93US-0158015.  
 PR 25-MAY-1995; 95US-0450257.  
 XX  
 XX (BARS/) BARSOUM J G.  
 PA (FAWE/) FAWELL S E.  
 PA (FRAN/) FRANKEL A.  
 PA (PABO/) PABO C.  
 PA (PEPI/) PEPINSKY R B.



Barsoum JG, Favell SE, Frankel A, Pabo C. Pepinsky RB.  
WPI; 1997-392943/36.

New DNA constructs for transporting molecules to cells - encode a fusion protein comprising a modified HIV tat protein and a carboxy-terminal cargo moiety

Example 13; Column 93: 76pp: English.

PCR primers EA21 (AAAT84579), and EA22 (AATB4580) were used to amplify bovine papillomavirus E2 repressor DNA from plasmid PCO-E2. EA21 introduces an NcoI site that adds a Met codon followed by an Ala codon 5' to the coding region for the C-terminal 101 residues of gpv-1 E2. The PCR product was used in the preparation of chemically cross-linked Tat-E2 conjugates. Novel transport proteins comprise a fusion between HIV tat protein, preferably deleted of its Cys-rich region and exon 2-encoded C-terminal region, and a cargo molecule. The tat moiety delivers the cargo molecule to cells in vivo or in vitro.

Sequence 27 BP: 8 A; 8 C; 7 G; 4 T; 0 other:

Best Match  
Query Local Similarity 13.0%; Score 15.6; DB 18; Length 27;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps

3 GATGCCCATAGTGCACCTCCTAA 24  
II IIIII IIIIII II II I  
6 GAAGCCATCGTGCACTGTCCCAA 27

RESULT 94  
ID ID AAAV56609 standard; DNA: 27 BP.

AAV56609:  
24-NOV-1998 (first entry)  
TAT-E2 conjugate primer EA-21.

TAT protein: cargo molecule: therapy: diagnosis: transport protein:  
fusion protein: human papillomavirus E2 repressor: target cell:  
primer: ss.

Synthetic:  
US5804604-A.  
08-SEP-1998.  
25-MAY-1995: 95U5-0450236.  
28-APR-1994: 94U5-0235403.  
21-DEC-1989: 89U5-0454450.  
02-JAN-1991: 91U5-0636662.  
19-AUG-1993: 93WO-US07833.  
24-NOV-1993: 93US-0158015.  
25-MAY-1995: 95US-0450236.  
(BTQ ) BIOGEN INC.

Barsoum JG, Favell SE, Frankel A, Pabo C. Pepinsky RB.  
WPI; 1998-505702/43.

HIV tat-derived transport fusion proteins - used to deliver biological active moieties e.g. peptides(s) or nucleic acids, specifically into cytoplasm or nuclei of cells

Example 13; Column 93-94: 83pp: English.

XX	AAV56597-V56610 are primers used in a method for the delivery of
CC	biologically active cargo molecules into the cytoplasm and nuclei of
CC	cells, for therapeutic, prophylactic or diagnostic purposes. This is
CC	accomplished by the presence of a small, basic section of the tat
CC	transport protein from human immunodeficiency virus (HIV) type 1. This
CC	is used as it is this protein which is observed to cause human cells in
CC	culture to take up HIV. The method involves the use of a cargo moiety in
CC	combination with a transport moiety usually in the form of a fusion
CC	protein. The cargo moiety is a human papillomavirus E2 repressor that
CC	retains its biological activity after delivery into a target cell and
CC	where the transport moiety is one of following HIV tat protein fragments
CC	(a) aa 4-38, (b) aa 47-72, (c) 38-72, (d) aa 38-58, (e) aa 37-58,
CC	(f) aa 1-21 and 38-72, (g) aa 47-62 or aa 38-62. The proteins allow
CC	delivery of specific peptides into cells at high concentrations due to
CC	use of existing transporters. Previous methods of delivery include
CC	bombardment and transforming, which only allow a fraction of the cell
CC	population to be infected and can additionally damage cells as they
CC	cause physical opening of the cell walls/membranes to allow entry.
XX	
SQ	Sequence 27 BP; 8 A; 8 C; 7 G; 4 T; 0 other;
	Query Match 13.0%; Score 15.6; DB 19; Length 27;
	Best Local Similarity 81.8%; Prod No. 4.6e+04;
	Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY	3 GATGCCACTAGTACCTCCTAA 24
	I I I I I I I I I I I I I I I I
DB	6 GAAGCCATGTCGTACTCCCA 27
	RESULT 95
AAD26641	
ID	AAD26641 standard: DNA: 27 BP.
AC	AAD26641:
AC	
DT	26-MAR-2002 (first entry)
DE	Bovine papillomavirus-16 E2 DNA fragment generating EX21 PCR primer.
KW	Human immunodeficiency virus: HIV-1; tat; therapeutic: toxin; enzyme;
KW	regulatory factor; prophylactic; extracellular fusion protein; drug;
KW	bovine papillomavirus-16; BPV-16; ss.
OS	Bovine papillomavirus.
PN	
PD	US6116003-B1.
PP	13-NOV-2001.
PI	28-APR-1994: 94US-0235403.
PR	02-JAN-1991: 91US-0636662.
PR	21-DEC-1989: 89US-0454450.
PR	21-AUG-1992: 92US-0934375.
PR	19-AUG-1993: 93WO-US07813.
PA	24-NOV-1993: 93WO-0158015.
PA	(WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA	(UXAO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
PA	(BIOL ) BIOGEN INC.
PI	Frankel A. Pabo C. Barsoum JG. Fawell SE. Pepinsky RB.
DP	WPI: 2002-088872/12.
DX	
PT	Delivering biologically active cargo molecules such as polypeptides,
PT	nucleic acids into cells by using transport polypeptides which comprise
PT	human immunodeficiency virus transactivator protein linked to cargo
PT	molecules .
XX	
XX	Example 13: Column 93: 2800. English

CC The invention relates to a method for delivering a biologically active  
 CC cargo molecule of interest into a cell. The method comprises presenting  
 CC to the cell an extracellular fusion protein or a covalently linked  
 CC conjugate consisting of a cargo moiety and a transport moiety having  
 CC amino acids 49-57 of human immunodeficiency virus (HIV) transactivator  
 CC (tat) protein and lacking amino acids 22-36 and 71-86 of HIV tat protein.  
 CC The method is useful for delivering a molecule of interest such as  
 CC polypeptides, antigen, monoclonal antibody, single- or double-stranded  
 CC nucleic acid, a therapeutic, prophylactic and diagnostic molecule to a  
 CC cell in vitro or in vivo. The method delivers proteins or peptides,  
 CC including regulatory factors, enzymes, drugs or toxins into the cytoplasm  
 CC and cell nucleus. The method is useful for diagnostic, prophylactic or  
 CC therapeutic intracellular delivery of small and macro molecules. The  
 CC present sequence is a PCR primer used for generating bovine  
 CC papillomavirus-16 (BPV-16) E2 protein used in the exemplification of  
 CC the invention.

XX Sequence 27 BP; 8 A; 8 C; 7 G; 4 T; 0 other;

Query Match 13.0% Score 15.6; DB 24; Length 27;

Best Local Similarity 81.8% Pred. No. 4.6e+04;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 GATCCATAGTACCTCTCTAA 24

DB 6 GAACCCATGCTGACTCTCCAA 27

RESULT 96

AAT38277/c

ID AAT38277 standard; DNA: 31 BP.

XX AC AAT38277

XX 29-DEC-1996 (first entry)

XX Murine 103 gene forward primer.

XX T helper cell; TH cell; T-cell; T-lymphocyte; 103 gene;  
 XX differential expression; immune disorder; multiple sclerosis;  
 XX asthma; lepromatous leprosy; diagnosis; therapy; primer; PCR;  
 XX polymerase chain reaction; IgG1; fusion protein; ss.

XX Synthetic.

XX WO9627603-A1.

XX 12-SEP-1996.

XX 01-MAR-1996; 96WO-US02798.

XX 07-JUN-1995; 95US-0487748.

XX 03-MAR-1995; 95US-0398633.

XX (MILL-) MILLENNIUM PHARM INC.

XX Levinson DA;

XX WPI; 1996-433404/43.

XX Genes and their products differentially expressed in T helper cells  
 XX - useful in diagnosis and treatment of immune disorders, e.g.  
 XX multiple sclerosis, asthma, lepromatous leprosy, etc.

XX Example 10; Page 163; 218pp; English.

XX A forward primer (AAT38277) and reverse primer (AAT38278) were used  
 XX to amplify DNA encoding the extracellular domain (but not the  
 XX signal peptide) of the murine 103 gene product. The 103 gene  
 XX (AAT38272) is differentially expressed in T helper TH2 cells. The  
 XX PCR product was used to construct a plasmid encoding a fusion  
 XX protein contg. the CD5 signal sequence, 103 extracellular domain

CC and human IgG1 heavy chain Fc region. This was expressed in  
 CC COS transfectants. The fusion proteins facilitate solubility  
 CC and/or expression, and can increase the blood half-life, of the  
 CC 103 gene product, a TH2 cell-specific surface marker.

XX Sequence 31 BP; 5 A; 8 C; 12 G; 6 T; 0 other;

Query Match 13.0% Score 15.6; DB 17; Length 31;

Best Local Similarity 70.0% Pred. No. 4.9e+04;

Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 42 CCATCCAGAGGATTTCAGGGTTCACGCG 71

DB 31 CCACCCAGGACGATTACTGGTACCCGCG 2

RESULT 97

AAA51910/c

ID AAA51910 standard; DNA: 31 BP.

XX AC AAA51910;

XX 31-OCT-2000 (first entry)

XX Forward primer for murine gene 103 fragment amplification.

XX T helper cell; differential expression; 200 gene; immunomodulator;  
 XX anti-inflammatory; anti-arthritis; antibacterial; immunosuppressive;  
 XX thrombinetic; anti-thyroid; anti-asthmatic; anti-allergic; antiviral;  
 XX protozoicide; lymphocyte; modulator; gene therapy; primer; ss.

XX Mus sp.

XX US6084083-A.

XX 04-JUL-2000.

XX 28-MAR-1997; 97US-0829525.

XX 01-MAR-1996; 96US-0609583.

XX 03-MAR-1995; 95US-0398633.

XX 07-JUN-1995; 95US-0487748.

XX (MILL-) MILLENNIUM PHARM INC.

XX Levinson DA;

XX WPI; 2000-464385/40.

XX New isolated human 200 gene products or polypeptides, useful for  
 XX treating and diagnosing immune disorders, especially T helper  
 XX lymphocyte-related disorders

XX Example; Column 89; 107pp; English.

XX AAA51910-11 were used to amplify the cDNA encoding extracellular domain  
 XX of the murine 103 gene. The amplified fragment was used to construct an  
 XX IgG1 fusion protein.

XX Genes which are differentially expressed within and among T helper (TH)  
 XX cells and TH cell subpopulations, e.g. TH0, TH1 and TH2 subpopulations,  
 XX can be used diagnostically or as targets for therapeutic intervention.

XX The polypeptides are useful for treating and diagnosing of immune  
 XX disorders, especially T lymphocyte-related disorders. These disorders  
 XX include chronic inflammatory diseases and disorders (e.g. Crohn's  
 XX disease, reactive arthritis, Lyme disease, Hashimoto's thyroiditis or  
 XX Grave's disease), or atopic conditions (e.g. asthma and allergy,

XX including allergic rhinitis or food allergies). Also included are  
 XX certain pathogen susceptibilities (e.g. leishmaniasis) and viral (e.g.  
 XX HIV) or bacterial (e.g. tuberculosis or lepromatous leprosy) infections.

XX Sequence 31 BP; 5 A; 8 C; 12 G; 6 T; 0 other;

Query Match

13.0% Score 15.6; DB 21; Length 31;

Best Local Similarity 70.0%; Pred. NO. 4.9e+04;  
Matches 21: Conservative 0; Mismatches 9; Indels 0; Gaps 0.

OY 42 CCACCTCCAGAGGATTCAGGGGTTCCAGCG 71  
||||| ||||| ||||| ||||| ||||| |||||  
DB 31 CCACCCAGGAGGATTTACTGGTACCCGCG 2

## RESULT 98

AAI70273/c  
ID AAI70273 standard: DNA: 31 BP.

XX AC AAI70273:

XX DT 07-JAN-2002 (first entry)

XX DE Mouse 103 gene forward PCR primer.

XX KW Mouse; 200 gene; T helper; T lymphocyte; T cell; TH2; IgG1;  
XX differential expression: immune disorder; diagnosis; therapy;  
XX PCR primer; ss.

XX OS Mus musculus.

XX PN US6288218-B1.

XX PD 11-SEP-2001.

XX PF 25-SEP-1997; 97US-0937399.

XX PR 01-MAR-1996; 96US-0609583.

XX PR 03-MAR-1995; 95US-0398633.

XX PR 07-JUN-1995; 95US-0487748.

XX PA (LEVI/) LEVINSON D A.

XX PI Levinson DA;

XX DR WPI: 2001-647189/74.

XX Detecting 200 gene expression in a sample, useful for treating and  
XX diagnosing immune disorders, especially T lymphocyte-related disorders,  
XX comprises detecting the presence of a 200 gene product or an RNA  
XX encoding the 200 gene product.

XX Example 10: Column 91: 108pp: English.

XX The present sequence is that of the forward primer (reverse primer  
XX given in AAI70274) used in the PCR amplification of a DNA fragment  
XX encoding the extracellular domain of the murine 203 gene (see  
XX AAI70257). The primers were designed to create a 5' KpnI site and  
XX a 3' BamHI site in the amplified fragment to facilitate insertion  
XX into plasmid pCDB-CD4-IgG1. The PCR product was used in the  
XX construction of a fusion comprising the CD5 signal sequence, 103  
XX gene product extracellular domain and the human IgG1 heavy chain Fc  
XX region. The murine 103 gene is preferentially expressed in the TH2  
XX cell subpopulation, and is one of a series of genes identified  
XX in the invention as being differentially expressed within and among  
XX in cells and TH cell subpopulations. Such genes can be used  
XX diagnostically or as targets for therapeutic invention, especially  
XX in the treatment of TH cell subpopulation-related disorders, such as  
XX multiple sclerosis, psoriasis and insulin-dependent diabetes (all  
XX claimed). (Thom S disease, reactive arthritis, Lyme disease,  
XX disease, contact dermatitis, graft rejection, graft versus host  
XX disease, sarcoidosis, asthma, allergy, allergic rhinitis, food  
XX allergy, eosinophilia, conjunctivitis, glomerular nephritis, and  
XX helminthiasis (e.g., leishmaniasis), viral (e.g., HIV) and bacterial  
XX (e.g., tuberculosis and lepromatous leprosy) infections.

XX Sequence 31 BP; 5 A; 8 C; 12 G; 6 T; 0 other;

Query Match 13.0%; Score 15.6; DB 22; Length 31;

Best Local Similarity 70.0%; Pred. NO. 4.9e+04;  
Matches 21: Conservative 0; Mismatches 9; Indels 0; Gaps 0.

OY 42 CCACCTCCAGAGGATTCAGGGGTTCCAGCG 71  
||||| ||||| ||||| ||||| ||||| |||||  
DB 31 CCACCCAGGAGGATTTACTGGTACCCGCG 2

## RESULT 99

AAO3380/c

ID AAO3380 standard: DNA: 31 BP

XX AC AAO3380:

XX DT 13-JUN-2001 (first entry)

XX DE 5' primer, to amplify murine 103 gene.

XX KW 103 gene; immune disorder; T helper lymphocyte 2 related disorder;  
XX TH2; ST2; T1; Fit-1; therapy; asthma; allergy; IgE; IL-4; antiviral;  
XX immunoglobulin E mediated condition; interleukin-4 mediated condition;  
XX Crohn's disease; arthritis; insulin-dependent diabetes; antihelminthic;  
XX multiple sclerosis; Hashimoto's thyroiditis; Grave's disease;  
XX contact dermatitis; psoriasis; allergic rhinitis; conjunctivitis;  
XX glomerular nephritis; systemic lupus erythematosus; eosinophilia;  
XX neuroprotective; ophthalmological; antibacterial; immunosuppressive;  
XX sarcoidosis; scleroderma; murine; PCR primer; ss.

XX OS Mus musculus.

XX PN WO200121641-A1.

XX PD 29-MAR-2001.

XX PF 25-SEP-2000; 2000WO-US26555.

XX PR 24-SEP-1999; 99US-0155862.

XX PR 28-APR-2000; 2000US-0560639.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Leiby KR, Kingsbury GA;

XX DR WPI: 2001-211462/21.

XX New 103 gene products and immunospecific antibodies, useful for the  
XX diagnosis and treatment of T helper lymphocyte 2 (like) related immune  
XX disorders e.g. asthma, allergy, immunoglobulin E and interleukin-4  
XX mediated conditions.

XX Example: Page 110: 197pp: English.

XX The invention relates to methods and compositions for treatment  
XX and diagnosis of immune disorders, especially T lymphocyte-related  
XX disorders. The methods and compositions of the present invention  
XX particularly relates to detection and/or modulation of expression  
XX and/or activity of 103 gene. This gene is alternatively referred  
XX as ST2, T1 and Fit-1 and is differentially expressed in T helper  
XX lymphocyte 2 (TH2) cells. Antibodies specific for 103 gene are  
XX useful for the treatment and prevention of immune disorders in  
XX humans, preferably TH2 related disorders, such as asthma, allergy,  
XX immunoglobulin E (IgE) mediated conditions and interleukin-4 (IL-4)  
XX mediated conditions. Modulators of 103 gene such as antibodies,  
XX ribozymes, antisense oligonucleotides and peptides are useful for  
XX the treatment and diagnosis of immune disorders such as Crohn's  
XX disease, arthritis, insulin-dependent diabetes, multiple sclerosis,  
XX Hashimoto's thyroiditis, Grave's disease, graft rejection, contact  
XX dermatitis, psoriasis, allergic rhinitis, conjunctivitis, graft-  
XX versus host disease, glomerular nephritis, sarcoidosis, eosinophilia,  
XX systemic lupus erythematosus, scleroderma and helminthic (e.g.  
XX leishmaniasis), viral and bacterial infections (e.g. tuberculosis  
XX and lepromatous leprosy).

XX The present sequence is 5' primer used to amplify a fragment



Db 8 CTCGATGCGCGGAATACAGTCAG 35

## RESULT 99

US-08-961-083-434  
; Sequence 434, Application US/08961083  
; Patent No. 6159469  
; GENERAL INFORMATION:  
; APPLICANT: Choi et. al.  
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
; NUMBER OF SEQUENCES: 452  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/08/961.083  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brockles A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 434:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 35 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-961-083-434

Query Match 12.7% Score 15.2; DB 3; Length 35;  
Best Local Similarity 85.0%; Pred. No. 8.7e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 22 TAACCCACACTTATCC 41  
Db 16 TAACCCACTTATCC 35

## RESULT 100

US-09-424-620B-6  
; Sequence 6, Application US/09424620B  
; Patent No. 6391585  
; GENERAL INFORMATION:  
; APPLICANT: HANIL SYNTHETIC FIBER CO., LTD.  
; JANG, Ki-Ryong  
; MOON, Jae-Woong  
; BAE, Cheon-Soon  
; YANG, Doo-Suk  
; LEE, Jee-Won  
; SEONG, Baik-Lin  
; TITLE OF INVENTION: Process for preparing recombinant proteins using highly  
; efficient expression vector from *Saccharomyces cerevisiae*  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BACHMAN & LAPOINTE, P.C.  
; STREET: Suite 1201, 900 Chapel Street  
; CITY: New Haven

STATE: Connecticut  
COUNTRY: U.S.A.  
ZIP: 06510-2802  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM  
OPERATING SYSTEM: WINDOWS 95/98  
SOFTWARE: MS WORD  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/424,620B  
FILING DATE: 24-No. 6391585-1999  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: oligonucleotide  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-424-620B-6  
Query Match 12.7% Score 15.2; DB 4; Length 36;  
Best Local Similarity 63.9%; Pred. No. 8.8e+03;  
Matches 23; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
Oy 56 TTCAGGGGTTCCAGCGTCTCTCGAAATGATCGATTG 91  
Db 1 TTATGAGCTCTATTGTGTATGAATGATGATTG 36  
Search completed: June 17, 2003, 21:38:30  
Job time : 68 secs

1 CURRENT APPLICATION DATA:  
2 APPLICATION NUMBER: US/08/558.823  
3 FILING DATE:  
4 CLASSIFICATION:  
5 ATTORNEY/AGENT INFORMATION:  
6 NAME: Rogalsky Esq., Peter  
7 REGISTRATION NUMBER: 38,601  
8 REFERENCE/DOCKET NUMBER: 19603/400  
9 TELECOMMUNICATION INFORMATION:  
10 TELEPHONE: (716) 263-1600  
11 TELEFAX: (716) 263-1634  
12 INFORMATION FOR SEQ ID NO: 11:  
13 SEQUENCE CHARACTERISTICS:  
14 LENGTH: 27 base pairs  
15 TYPE: nucleic acid  
16 STRANDEDNESS: single  
17 TOPOLOGY: linear  
18 MOLECULE TYPE: cDNA  
19 US-08-558-823-11

Query Match 12.7% Score 15.2; DB 2; Length 27;  
Best Local Similarity 58.3%; Pred. No. 7.9e+03;  
Matches 14; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 31 CCTCATATCCCACTCCAGAGG 54  
Db 24 CAYAAATMYCAYCTAGAGG 1

RESULT 97  
US-08-943-731-565  
Sequence 565, Application US/08943731  
Patent No. 6265157  
GENERAL INFORMATION:  
APPLICANT: PROCKOP, DARIN J.  
APPLICANT: SPOTILA, LORETTA D.  
APPLICANT: DELTAS, CONSTANTINOS D.  
APPLICANT: SEREDA, LARISA  
APPLICANT: LARSON, ANDREA W.  
APPLICANT: PACK, MICHAEL  
APPLICANT: COLIGE, ALAIN  
APPLICANT: EARLY, JAMES  
APPLICANT: FORKKO, JARMO  
APPLICANT: ALA-KORKO, LEENA, et al.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING  
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES  
NUMBER OF SEQUENCES: 666  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND  
STREET: FLA.  
CITY: PHILADELPHIA  
STATE: PA  
COUNTRY: USA  
ZIP: 19103-7086  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943.731  
FILING DATE: 03-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/212.322  
FILING DATE: 14-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/803.628  
FILING DATE: 03-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: DOYLE LEARY PH.D., KATHRYN  
REGISTRATION NUMBER: 36,517

1 REFERENCE/DOCKET NUMBER: 9598-27  
2 TELECOMMUNICATION INFORMATION:  
3 TELEPHONE: 215-965-1284  
4 TELEFAX: 215-567-2991  
5 TELEX: 831-494  
6 INFORMATION FOR SEQ ID NO: 565:  
7 SEQUENCE CHARACTERISTICS:  
8 LENGTH: 28 base pairs  
9 TYPE: nucleic acid  
10 STRANDEDNESS: single  
11 TOPOLOGY: linear  
12 MOLECULE TYPE: DNA (genomic)  
13 US-08-943-731-565

Query Match 12.7% Score 15.2; DB 4; Length 28;  
Best Local Similarity 85.0%; Pred. No. 8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 16 CCTCTTAACCCACACTCA 35  
Db 8 CCTCTTATCCACAGCACA 27

RESULT 98  
US-08-727-449-3  
Sequence 3, Application US/08727449  
Patent No. 5932435  
GENERAL INFORMATION:  
APPLICANT: Atkins, David  
APPLICANT: Izant, Greg M.  
TITLE OF INVENTION: AN IN VIVO GENE EXPRESSION SYSTEM  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/727.449  
FILING DATE: OCTOBER 18, 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PWS169/94 (AUSTRALIA)  
FILING DATE: 20-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1012/51992-PCT-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-727-449-3

Query Match 12.7% Score 15.2; DB 2; Length 35;  
Best Local Similarity 71.4%; Pred. No. 8.7e+03;  
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 93 CTTCCATAGCTGCTGAATTCAGTTT 120  
||||| ||| ||| ||| ||| ||| ||| |||

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 05/08/687,421  
FILING DATE: 08-MAY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/195,005  
FILING DATE: 10-FEBRUARY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE: 22-APRIL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/219,012  
FILING DATE: 28-MARCH-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/973,333  
FILING DATE: 11-NOVEMBER-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX07/PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 146:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 base pairs  
TOPOLG: 30 base pairs  
STRANDEDNESS: single  
TOPOLG: linear  
FEATURE:  
OTHER INFORMATION: All C's are 2'-NH2 cytosine  
FEATURE:  
OTHER INFORMATION: All U's are 2'-NH2 uracil  
US-08-687-421-146

Query Match 12.84; Score 15.4; DB 4; Length 50;  
Best Local Similarity 94.18; Pred. No. 8.4e-03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 16 CCCTCTTACCCACCC 32  
Db 47 CCCTCTTACCCACCC 31

RESULT 95  
US-08-687-421-184/c  
Sequence 184, Application US/08687421  
Patent No. 6177557  
GENERAL INFORMATION:  
APPLICANT: Gold, Larry  
APPLICANT: Janjic, Nebojsa  
APPLICANT: Tasset, Diane  
TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC  
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND  
TITLE OF INVENTION: THROMBIN  
NUMBER OF SEQUENCES: 445  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/687,421  
FILING DATE: 08-MAY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/195,005  
FILING DATE: 10-FEBRUARY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE: 22-APRIL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/219,012  
FILING DATE: 28-MARCH-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/973,333  
FILING DATE: 11-NOVEMBER-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX07/PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 184:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 base pairs  
TOPOLG: 30 base pairs  
STRANDEDNESS: single  
TOPOLG: linear  
FEATURE:  
OTHER INFORMATION: All C's are 2'-NH2 cytosine  
FEATURE:  
OTHER INFORMATION: All U's are 2'-NH2 uracil  
US-08-687-421-184

Query Match 12.84; Score 15.4; DB 4; Length 50;  
Best Local Similarity 94.18; Pred. No. 8.4e-03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 16 CCCTCTTACCCACCC 32  
Db 47 CCCTCTTACCCACCC 31

RESULT 96  
US-08-558-823-11/c  
Sequence 11, Application US/08558823  
Patent No. 5876994  
GENERAL INFORMATION:  
APPLICANT: Knipple, Douglas C.  
APPLICANT: Roelofs, Wendell L.  
APPLICANT: Miller, Stuart J.  
TITLE OF INVENTION: PHEROMONE DESATURASES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

APPLICANT: Janjic, Nebojsa  
TITLE OF INVENTION: High-Affinity RNA Ligands of Basic  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/384,708A

FILING DATE: 02-FEBRUARY-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/195,005

FILING DATE: 10-FEBRUARY-1994

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: NEX07/D

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3433

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 146:

SEQUENCE CHARACTERISTICS:

LENGTH: 50 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

OTHER INFORMATION: All C's are 2'-NH2 cytosine

OTHER INFORMATION: All U's are 2'-NH2 uracil

US-08-384-708A-146

Query Match 12.8%; Score 15.4; DB 1; Length 50;  
Best Local Similarity 94.1%; Pred. No. 8.4e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 16 CCCTCCTAACCCACACC 32

Db 47 CCCTCCTTACCCACACC 31

RESULT 93

US-08-384-708A-184/c

Sequence 184; Application US/08384708A

Patent No. 5639868

GENERAL INFORMATION:

APPLICANT: Gold, Larry

APPLICANT: Janjic, Nebojsa

TITLE OF INVENTION: High-Affinity RNA Ligands of Basic

TITLE OF INVENTION: Fibroblast Growth Factors

NUMBER OF SEQUENCES: 227

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200

CITY: Englewood

STATE: Colorado

COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/384,708A  
FILING DATE: 02-FEBRUARY-1995  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/195,005

FILING DATE: 10-FEBRUARY-1994

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428

FILING DATE: 11-JUNE-1990

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: NEX07/D

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3433

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 184:

SEQUENCE CHARACTERISTICS:

LENGTH: 50 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

OTHER INFORMATION: All C's are 2'-NH2 cytosine

OTHER INFORMATION: All U's are 2'-NH2 uracil

US-08-384-708A-184

Query Match 12.8%; Score 15.4; DB 1; Length 50;  
Best Local Similarity 94.1%; Pred. No. 8.4e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 16 CCCTCCTAACCCACACC 32

Db 47 CCCTCCTTACCCACACC 31

RESULT 94

US-08-687-421-146/c

Sequence 146; Application US/08687421

Patent No. 6177557

GENERAL INFORMATION:

APPLICANT: Gold, Larry

APPLICANT: Janjic, Nebojsa

APPLICANT: Tasset, Diane

TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC

TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND

TITLE OF INVENTION: THROMBIN

NUMBER OF SEQUENCES: 445

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200

CITY: Englewood

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 6.0







APPLICANT: Luma, William C. Jr.  
APPLICANT: Sisko, John T.  
APPLICANT: Smith, Anthony M.  
APPLICANT: Stokker, Gerald E.  
APPLICANT: Tucker, Thomas J.  
TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
FILE REFERENCE: 20393Y  
CURRENT APPLICATION NUMBER: US/09/516,750  
CURRENT FILING DATE: 2000-03-01  
EARLIER APPLICATION NUMBER: 60/122,768  
EARLIER FILING DATE: 1998-03-03  
EARLIER APPLICATION NUMBER: 60/127,253  
EARLIER FILING DATE: 1999-03-31  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 42  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: completely synthetic sequence  
US-09-516-750-5

Query Match 12.8% Score 15.4; DB 4; Length 42;  
Best Local Similarity 66.7% Pred. No. 7.9e+03;  
Matches 22: Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 44 ACTCAGAGGATTCAGGGGTTCCAGCGTTCT 76  
| | | | | | | | | | | | | | | | | | | |  
DB 6 AGCTAGAGTTAACCCGGTGTCCCGGTTGCT 38

RESULT 82  
US-09-342-577-6  
Sequence 6, Application US/09/342577  
Patent No. 6358985  
GENERAL INFORMATION:  
APPLICANT: Merck & Co., Inc.  
APPLICANT: Anthony, Neville J.  
APPLICANT: Bell, Ian M.  
APPLICANT: Beshore, Douglas C.  
APPLICANT: Ciccarone, Terrence M.  
APPLICANT: Desolma, S. Jane  
APPLICANT: Dinsmore, Christopher J.  
APPLICANT: Stokker, Gerald E.  
TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN  
FILE REFERENCE: 20275Y  
CURRENT APPLICATION NUMBER: US/09/342,577  
CURRENT FILING DATE: 1999-06-29  
EARLIER APPLICATION NUMBER: 60/091,513  
EARLIER FILING DATE: 1998-07-02  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 42  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: completely synthetic sequence  
US-09-342-577-6

Query Match 12.8% Score 15.4; DB 4; Length 42;  
Best Local Similarity 66.7% Pred. No. 7.9e+03;  
Matches 22: Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 44 ACTCAGAGGATTCAGGGGTTCCAGCGTTCT 76  
| | | | | | | | | | | | | | | | | | | |  
DB 6 AGCTAGAGTTAACCCGGTGTCCCGGTTGCT 38

RESULT 83  
US-09-516-756-5

Sequence 5, Application US/09516756  
Patent No. 6376496  
GENERAL INFORMATION:  
APPLICANT: Merck & Co., Inc.  
APPLICANT: Hartman, George D.  
APPLICANT: Luma, William C. Jr.  
APPLICANT: Sisko, John T.  
APPLICANT: Smith, Anthony M.  
APPLICANT: Tucker, Thomas J.  
APPLICANT: Beigman, Jeffrey M.

TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
FILE REFERENCE: 20288Y  
CURRENT APPLICATION NUMBER: US/09/516,756  
CURRENT FILING DATE: 2000-03-01  
EARLIER APPLICATION NUMBER: 60/122,968  
EARLIER FILING DATE: 1998-03-03  
EARLIER APPLICATION NUMBER: 60/127,132  
EARLIER FILING DATE: 1999-03-31  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 42  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: completely synthetic sequence  
US-09-516-756-5

Query Match 12.8% Score 15.4; DB 4; Length 42;  
Best Local Similarity 66.7% Pred. No. 7.9e+03;  
Matches 22: Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 44 ACTCAGAGGATTCAGGGGTTCCAGCGTTCT 76  
| | | | | | | | | | | | | | | | | | | |  
DB 6 AGCTAGAGTTAACCCGGTGTCCCGGTTGCT 38

RESULT 84  
US-09-828-061A-6  
Sequence 6, Application US/09828061A  
Patent No. 6380228  
GENERAL INFORMATION:  
APPLICANT: Merck & Co., Inc.  
APPLICANT: Craig A. Stump  
APPLICANT: Theresa M. Williams  
TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
FILE REFERENCE: 20635Y  
CURRENT APPLICATION NUMBER: US/09/828,061A  
CURRENT FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: 60/196,231  
PRIOR FILING DATE: 2000-04-10  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 42  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Sense Nucleotide Sequence  
US-09-828-061A-6

Query Match 12.8% Score 15.4; DB 4; Length 42;  
Best Local Similarity 66.7% Pred. No. 7.9e+03;  
Matches 22: Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 44 ACTCAGAGGATTCAGGGGTTCCAGCGTTCT 76  
| | | | | | | | | | | | | | | | | | | |  
DB 6 AGCTAGAGTTAACCCGGTGTCCCGGTTGCT 38

RESULT 85  
US-09-463-917-5  
Sequence 5, Application US/09463917

Patent No. 6333335  
: GENERAL INFORMATION:  
: APPLICANT: Merck & Co., Inc.  
: APPLICANT: Dinsmore, Christopher J.  
: APPLICANT: Graham, Samuel L.  
: APPLICANT: Williams, Theresa M.  
: TITLE OF INVENTION: PRENYL-PROTEIN TRANSFERASE INHIBITORS  
: FILE REFERENCE: 20488  
: CURRENT APPLICATION NUMBER: US/08/609,205  
: CURRENT FILING DATE: 2000-06-30  
: PRIOR FILING DATE: 1999-07-23  
: NUMBER OF SEQ ID NOS: 24  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 6  
: LENGTH: 42  
: TYPE: DNA  
: ORGANISM: Artificial Sequence  
: FEATURE:  
: OTHER INFORMATION: completely synthetic sequence  
US-09-609-205-6

Query Match 12.8% Score 15.4; DB 4; Length 42;  
Best Local Similarity 66.7% Pred. No. 7.9e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
Qy 44 ACTCCAGAGGATTCAGGGGTTCCAGCGTTCCT 76  
||| ||| | | | | | | | | | | | | | | | |  
Db 6 AGCTAGAGTTAACCCGTCGTCGCCGCGTTCCT 38

RESULT 78  
US-09-516-945-5  
: Sequence 5, Application US/09516945  
: Patent No. 6335343  
: GENERAL INFORMATION:  
: APPLICANT: Merck & Co., Inc.  
: APPLICANT: Luma, William C. Jr.  
: APPLICANT: Smith, Anthony M.  
: APPLICANT: Sisko, John T.  
: TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
: FILE REFERENCE: 20335Y  
: CURRENT APPLICATION NUMBER: US/09/516,945  
: CURRENT FILING DATE: 2000-03-01  
: EARLIER APPLICATION NUMBER: 60/122,970  
: EARLIER FILING DATE: 1998-03-03  
: EARLIER APPLICATION NUMBER: 60/127,259  
: EARLIER FILING DATE: 1999-03-31  
: NUMBER OF SEQ ID NOS: 21  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 5  
: LENGTH: 42  
: TYPE: DNA  
: ORGANISM: Artificial Sequence  
: FEATURE:  
: OTHER INFORMATION: completely synthetic sequence  
US-09-516-945-5

Query Match 12.8% Score 15.4; DB 4; Length 42;  
Best Local Similarity 66.7% Pred. No. 7.9e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
Qy 44 ACTCCAGAGGATTCAGGGGTTCCAGCGTTCCT 76  
||| ||| | | | | | | | | | | | | | | | |  
Db 6 AGCTAGAGTTAACCCGTCGTCGCCGCGTTCCT 38

RESULT 79  
US-09-757-218-6  
: Sequence 6, Application US/09757218  
: Patent No. 6350755  
: GENERAL INFORMATION:  
: APPLICANT: Merck & Co., Inc.

APPLICANT: S. Jane deSolms  
: APPLICANT: Anthony W. Shaw  
: TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
: FILE REFERENCE: 20613  
: CURRENT APPLICATION NUMBER: US/09/757,218  
: CURRENT FILING DATE: 2001-01-09  
: PRIOR APPLICATION NUMBER: 60/175,703  
: PRIOR FILING DATE: 2000-01-12  
: NUMBER OF SEQ ID NOS: 25  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 6  
: LENGTH: 42  
: TYPE: DNA  
: ORGANISM: Artificial Sequence  
: FEATURE:  
: OTHER INFORMATION: Artificial Nucleotide Sequence  
US-09-757-218-6

Query Match 12.8% Score 15.4; DB 4; Length 42;  
Best Local Similarity 66.7% Pred. No. 7.9e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
Qy 44 ACTCCAGAGGATTCAGGGGTTCCAGCGTTCCT 76  
||| ||| | | | | | | | | | | | | | | | |  
Db 6 AGCTAGAGTTAACCCGTCGTCGCCGCGTTCCT 38

RESULT 80  
US-09-516-757-5  
: Sequence 5, Application US/09516757  
: Patent No. 635843  
: GENERAL INFORMATION:  
: APPLICANT: Merck & Co., Inc.  
: APPLICANT: Luma, William C. Jr.  
: APPLICANT: Sisko, John T.  
: APPLICANT: Smith, Anthony M.  
: APPLICANT: Tucker, Thomas J.  
: APPLICANT: Bergman, Jeffrey M.  
: APPLICANT: Dinsmore, Christopher J.  
: TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
: FILE REFERENCE: 20399Y  
: CURRENT APPLICATION NUMBER: US/09/516,757  
: CURRENT FILING DATE: 2000-03-01  
: EARLIER APPLICATION NUMBER: 60/122,771  
: EARLIER FILING DATE: 1998-03-03  
: EARLIER APPLICATION NUMBER: 60/127,257  
: EARLIER FILING DATE: 1999-03-31  
: NUMBER OF SEQ ID NOS: 21  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 5  
: LENGTH: 42  
: TYPE: DNA  
: ORGANISM: Artificial Sequence  
: FEATURE:  
: OTHER INFORMATION: completely synthetic sequence  
US-09-516-757-5

Query Match 12.8% Score 15.4; DB 4; Length 42;  
Best Local Similarity 66.7% Pred. No. 7.9e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
Qy 44 ACTCCAGAGGATTCAGGGGTTCCAGCGTTCCT 76  
||| ||| | | | | | | | | | | | | | | | |  
Db 6 AGCTAGAGTTAACCCGTCGTCGCCGCGTTCCT 38

RESULT 81  
US-09-516-750-5  
: Sequence 5, Application US/09516750  
: Patent No. 6358956  
: GENERAL INFORMATION:  
: APPLICANT: Merck & Co., Inc.  
: APPLICANT: Hartman, George D.

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/221,844  
FILING DATE: 29-DEC-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/718,738  
FILING DATE: 18-SEP-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/463,382  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/460,104  
FILING DATE: 02-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03323  
FILING DATE: 17-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: MILLONIG, ROBERT C.  
REGISTRATION NUMBER: 14,395  
REFERENCE/DOCKET NUMBER: 1488.0730004/EKS/RCH/SCW  
TELEPHONE: (202) 371-2400  
TELEFAX: (202) 371-2440  
INFORMATION FOR SEQ ID NO. 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-221-844-8

Query Match 12.8% Score 15.4; DB 4; Length 42;  
Best Local Similarity 61.0%; Pred. No. 7.9e+03;  
Matches 25; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
DB 1 CAGTGTACCCGCGCCAGGTAGTGGTCAGTGGCCACCA 41  
58 CAGCGGTTCACGGTTCCTCGAATGTGATGTTGGTTCCA 98  
||||| ||| | | | | | | | | | | | | | |

RESULT 74  
US-09-456-153-5  
Sequence 5, Application US/09456153  
Patent No. 6284755  
GENERAL INFORMATION:  
APPLICANT: deSolms, S. Jane  
APPLICANT: Graham, Samuel L.  
APPLICANT: Shaw, Anthony W.  
APPLICANT: Ciccarone, Terrence M.  
TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN  
FILE REFERENCE: 20312Y  
CURRENT APPLICATION NUMBER: US/09/456,153  
CURRENT FILING DATE: 1999-12-07  
EARLIER APPLICATION NUMBER: US 60/111,416  
EARLIER FILING DATE: 1998-12-08  
EARLIER APPLICATION NUMBER: US 60/129,282  
EARLIER FILING DATE: 1999-04-14  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO. 5  
LENGTH: 42  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: completely synthesized  
US-09-456-153-5

Query Match 12.8% Score 15.4; DB 4; Length 42;  
Best Local Similarity 66.7%; Pred. No. 7.9e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 44 ACTCCAGAGGATTCAGGGGTTCCAGCGTTCT 76  
| | | | | | | | | | | | | | | | | | | |  
DB 6 AGTCTAGAGTTAACCCGTTGTCGCCGCGTTGCT 38

RESULT 75  
US-09-455-627-5  
Sequence 5, Application US/09455627  
Patent No. 6316436  
GENERAL INFORMATION:  
APPLICANT: deSolms, S. Jane  
APPLICANT: Shaw, Anthony W.  
TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN  
FILE REFERENCE: 20325  
CURRENT APPLICATION NUMBER: US/09/455,627  
CURRENT FILING DATE: 1999-12-07  
EARLIER APPLICATION NUMBER: US 60/111,621  
EARLIER FILING DATE: 1998-12-08  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO. 5  
LENGTH: 42  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: completely synthesized  
US-09-455-627-5

Query Match 12.8% Score 15.4; DB 4; Length 42;  
Best Local Similarity 66.7%; Pred. No. 7.9e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 44 ACTCCAGAGGATTCAGGGGTTCCAGCGTTCT 76  
| | | | | | | | | | | | | | | | | | | |  
DB 6 AGTCTAGAGTTAACCCGTTGTCGCCGCGTTGCT 38

RESULT 76  
US-09-426-533-5  
Sequence 5, Application US/09426533  
Patent No. 6329376  
GENERAL INFORMATION:  
APPLICANT: Beigman, Jeffrey M.  
TITLE OF INVENTION: Inhibitors Of Prenyl-Protein Transferase  
FILE REFERENCE: 20289  
CURRENT APPLICATION NUMBER: US/09/426,533  
CURRENT FILING DATE: 1999-10-26  
EARLIER APPLICATION NUMBER: 60/101,177  
EARLIER FILING DATE: 1998-10-29  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO. 5  
LENGTH: 42  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: completely synthesized  
US-09-426-533-5

Query Match 12.8% Score 15.4; DB 4; Length 42;  
Best Local Similarity 66.7%; Pred. No. 7.9e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 44 ACTCCAGAGGATTCAGGGGTTCCAGCGTTCT 76  
| | | | | | | | | | | | | | | | | | | |  
DB 6 AGTCTAGAGTTAACCCGTTGTCGCCGCGTTGCT 38

RESULT 77  
US-09-609-205-6  
Sequence 6, Application US/09609205

STREET: 444 SO. FLOWER STREET, SUITE 200  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/07149  
FILING DATE: 19910927  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CAMPBELL, CATHRYN A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P31 8882  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-535-9001  
TELEFAX: 619-535-8949  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US91-07149-55

Query Match 12.8%; Score 15.4; DB 5; Length 39;  
Best Local Similarity 66.7%; Pred. No. 7.7e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 80 AATGATGCTTCCATAGCTGCTGAATTG 112  
Db 5 AAATACCTATTGCTACGCGCGCTGGATTG 37

RESULT 71  
US-08-718-738-8  
Sequence 8, Application US/08718738  
Patent No. 6013469  
GENERAL INFORMATION:  
APPLICANT: KUNSCHE, CHARLES A  
APPLICANT: CHOPRA, ARVIND  
APPLICANT: ROSEN, CRAIG A  
TITLE OF INVENTION: HUMAN B-CELL TRANSLOCATION GENES-2 AND 3  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/718.738  
FILING DATE: 18-SEP-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0730003/EKS/KNT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-718-738-8

Query Match 12.8%; Score 15.4; DB 3; Length 42;  
Best Local Similarity 61.0%; Pred. No. 7.9e+03;  
Matches 25; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Oy 58 CAGGGTTCCAGCGTTCTCGAAATGATCGATTGCTTCCA 98  
Db 1 CAGTGTACACGCGCCAGGTAGATGCTGCGCCAGCA 41

RESULT 72  
US-09-332-769-5  
Sequence 5, Application US/09332769  
Patent No. 6172076  
GENERAL INFORMATION:  
APPLICANT: Embrey, Mark W.  
APPLICANT: Perlow, Debra S.  
APPLICANT: Wal, John S.  
APPLICANT: Hoffman, Jacob M.  
TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN  
TITLE OF INVENTION: TRANSFERASE  
FILE REFERENCE: 199821  
CURRENT APPLICATION NUMBER: US/09/332.769  
CURRENT FILING DATE: 1999-06-14  
EARLIER APPLICATION NUMBER: US 60/089.311  
EARLIER FILING DATE: 1998-06-15  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 42  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: completely synthesized  
US-09-332-769-5

Query Match 12.8%; Score 15.4; DB 4; Length 42;  
Best Local Similarity 66.7%; Pred. No. 7.9e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 44 ACTCCAGGCGATTACGGGTTCCAGCGTTCTTCT 76  
Db 6 AGCTAGAGTTACCCGTCGCGCGGCTTGTCT 38

RESULT 73  
US-09-221-844-8  
Sequence 8, Application US/09221844  
Patent No. 6258777  
GENERAL INFORMATION:  
APPLICANT: KUNSCHE, CHARLES A  
APPLICANT: CHOPRA, ARVIND  
APPLICANT: ROSEN, CRAIG A  
TITLE OF INVENTION: HUMAN B-CELL TRANSLOCATION GENES-2 AND 3  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

US-09-158-767-6  
Sequence 6, Application US/09158767A  
Patent No. 6180363  
GENERAL INFORMATION:  
APPLICANT: Batard, Yannick  
INVENTOR: Batard, Yannick  
APPLICANT: Durst, Francis  
APPLICANT: Wark-Reichert, Daniele  
TITLE OF INVENTION: RECODING OF DNA SEQUENCES PERMITTING  
TITLE OF INVENTION: EXPRESSION IN YEAST AND OBTAINED TRANSFORMED YEAST  
FILE REFERENCE: A32000  
CURRENT APPLICATION NUMBER: US/09/158-767A  
CURRENT FILING DATE: 1998-09-23  
EARLIER APPLICATION NUMBER: FR 97-12094  
EARLIER FILING DATE: 1997-09-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 39  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURES: See also sequence listing  
OTHER INFORMATION: Synthetic primer  
US-09-158-767-6

Query Match 12.8% Score 15.4; DB 4; Length 39;  
Best Local Similarity 66.7%; Pred. No. 7.7e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 68 AGCGTCTCGAATGATCGATGCGTTCATA 100  
II IIII I I IIII IIII I I I  
DB 6 AGATTCAGTTAAGCTCGATGCGTTCGACA 38

RESULT 68  
US-08-367-685-27  
Sequence 27, Application US/08367685  
Patent No. 6258530  
GENERAL INFORMATION:  
APPLICANT: Huse, William D.  
TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF  
TITLE OF INVENTION: RANDOMIZED PEPTIDES  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: California  
COUNTRY: United States  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/07141  
FILING DATE: 19910927  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P31 9072  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US91-07141-27

Query Match 12.8% Score 15.4; DB 5; Length 39;  
Best Local Similarity 66.7%; Pred. No. 7.7e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 80 AATGATCGATGCTTCATGCTGCTGAATTG 112  
II IIII I I IIII IIII I I I  
DB 5 AAATACCTATTGCTACGGCAGCGCTGGATTG 37

RESULT 70  
PCT-US91-07141-55  
Sequence 55, Application PC/TUS9107149  
GENERAL INFORMATION:  
APPLICANT: HUSE, WILLIAM D.  
TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF  
TITLE OF INVENTION: HETEROMERIC RECEPTORS  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRETTY, SCHROEDER, BRUEGEMANN & CLARK

US-08-367-685-27  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-367-685-27

Query Match 12.8% Score 15.4; DB 4; Length 39;  
Best Local Similarity 66.7%; Pred. No. 7.7e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 80 AATGATCGATGCTTCATGCTGCTGAATTG 112  
II IIII I I IIII IIII I I I  
DB 5 AAATACCTATTGCTACGGCAGCGCTGGATTG 37

RESULT 69  
PCT-US91-07141-27  
Sequence 27, Application PC/TUS9107141;  
GENERAL INFORMATION:  
APPLICANT: Huse, William D.  
TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF  
TITLE OF INVENTION: RANDOMIZED PEPTIDES  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: California  
COUNTRY: United States  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/07141  
FILING DATE: 19910927  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P31 9072  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US91-07141-27

Query Match 12.8% Score 15.4; DB 5; Length 39;  
Best Local Similarity 66.7%; Pred. No. 7.7e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 80 AATGATCGATGCTTCATGCTGCTGAATTG 112  
II IIII I I IIII IIII I I I  
DB 5 AAATACCTATTGCTACGGCAGCGCTGGATTG 37

RESULT 70  
PCT-US91-07141-55  
Sequence 55, Application PC/TUS9107149  
GENERAL INFORMATION:  
APPLICANT: HUSE, WILLIAM D.  
TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF  
TITLE OF INVENTION: HETEROMERIC RECEPTORS  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRETTY, SCHROEDER, BRUEGEMANN & CLARK

ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/440,787A  
FILING DATE: 15-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/978,893  
FILING DATE: 10-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-IX 1586  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-440-787A-27

Query Match 12.8% Score 15.4; DB 1; Length 39;  
Best Local Similarity 66.7%; Pred. No. 7.7e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 80 AATGATCGATTGGCTCCATAGCTGCTGAATTG 112  
||| ||||| ||| ||||| |||||  
DB 5 AATACCTATTGCTACGCGCCGCTGGATTG 37

RESULT 65  
US-08-349-131-55  
Sequence 55, Application US/08349131  
Patent No. 5871974  
GENERAL INFORMATION:  
APPLICANT: HUSE, WILLIAM D.  
TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRETTY, SCHROEDER, BRURGEMANN & CLARK  
STREET: 444 SO. FLOWER STREET, SUITE 200  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/349,131  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/120,648  
FILING DATE:  
APPLICATION NUMBER: US/07/767,136  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: CAMPBELL, CATHRYN A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-IX 8882  
TELEPHONE: 619-535-9001  
TELEFAX: 619-535-8949  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-349-131-55

Query Match 12.8% Score 15.4; DB 2; Length 39;  
Best Local Similarity 66.7%; Pred. No. 7.7e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 80 AATGATCGATTGGCTCCATAGCTGCTGAATTG 112  
||| ||||| ||| ||||| |||||  
DB 5 AATACCTATTGCTACGCGCCGCTGGATTG 37

RESULT 66  
US-08-470-297A-55  
Sequence 55, Application US/08470297A  
Patent No. 6027533  
GENERAL INFORMATION:  
APPLICANT: HUSE, WILLIAM D.  
TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL & FLORES LLP  
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
CITY: SAN DIEGO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/470,297A  
FILING DATE: June 5, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CAMPBELL, CATHRYN A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-IX 1611  
TELEPHONE: 619-535-9001  
TELEFAX: 619-535-8949  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-470-297A-55

Query Match 12.8% Score 15.4; DB 3; Length 39;  
Best Local Similarity 66.7%; Pred. No. 7.7e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 80 AATGATCGATTGGCTCCATAGCTGCTGAATTG 112  
||| ||||| ||| ||||| |||||  
DB 5 AATACCTATTGCTACGCGCCGCTGGATTG 37

RESULT 67



APPLICANT: Allison, Lori A.  
APPLICANT: Carrier, Helaine  
APPLICANT: Konevski, Ivan  
TITLE OF INVENTION: DNA Constructs and Methods for Stably  
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and  
TITLE OF INVENTION: Expressing Recombinant Proteins Therein  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
STREET: 1601 Market Street Suite 720  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103-2107  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/193,853  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
PRIORITY NUMBER: 08/189,256  
PRIORITY DATE:  
PRIORITY INVENTION DATA:  
PRIORITY NUMBER: US 07/518,763  
PRIORITY DATE: 01-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Reed, Janet E.  
REGISTRATION NUMBER: 36,252  
TELEPHONE: (215) 563-4100  
TELEFAX: (215) 563-4044  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-193-853-46  
Query Match 12.8% Score 15.4; DB 4; Length 33;  
Best Local Similarity 76.0%; Pred. No. 7.2e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
CY 5 TGCCATGATGACCTCTCAACCCAC 29  
DB 9 TTCCATGGTGATCTCTATTCAAC 33  
RESULT 62  
US-09-245-338-6  
Sequence 6, Application US/09249338  
Patent No. 6214589  
GENERAL INFORMATION:  
APPLICANT: Nippon Shokubai Co., Ltd.  
TITLE OF INVENTION: Method for Producing L-aspartic acid  
FILE REFERENCE: PH-612  
CURRENT APPLICATION NUMBER: US/09/249,338  
CURRENT FILING DATE: 1999-02-12  
EARLIER APPLICATION NUMBER: JP 98/31809  
EARLIER FILING DATE: 1998-2-13  
NUMBER OF SEQ ID NOS: 8  
SEQ ID NO 9  
LENGTH: 37  
MEDIUM TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Designed primer based on aspartase gene sequence of Pseudomonas  
OTHER INFORMATION: fluorescens IFU 3081 strain  
US-09-249-338-6  
Query Match 12.8% Score 15.4; DB 4; Length 37;  
Best Local Similarity 66.7%; Pred. No. 7.5e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
CY 40 CCCCATCCAGAGGATTCAGGCGTTCCAGCGT 72  
DB 1 CCCCATCCCTTAGGCGCTTCAGCGGCAAGCGT 33  
RESULT 63  
US-08-464-136-55  
Sequence 55, Application US/08464136  
Patent No. 5698426  
GENERAL INFORMATION:  
APPLICANT: HUSE, WILLIAM D.  
TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF  
TITLE OF INVENTION: HETEROMERIC RECEPTORS  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRETTI, SCHROEDER, BRUEGGEMANN & CLARK  
STREET: 444 SO. FLOWER STREET, SUITE 200  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,136  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CAMPBELL, CATHRYN A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P31 8892  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-535-9001  
TELEFAX: 619-535-8949  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-464-136-55  
Query Match 12.8% Score 15.4; DB 1; Length 39;  
Best Local Similarity 66.7%; Pred. No. 7.7e+03;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
CY 80 AATCATGATGGCTTCATAGCTGCTGATTC 112  
DB 5 AATACCTATTGCTACGCGAGCCCTGGATTG 37  
RESULT 64  
US-08-440-787A-27  
Sequence 27, Application US/08440787A  
Patent No. 5770434  
GENERAL INFORMATION:  
APPLICANT: Huse, William D.  
TITLE OF INVENTION: Soluble Peptides Having Constrained,  
TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making  
NUMBER OF SEQUENCES: 174  
CORRESPONDENCE ADDRESS:

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/09/380.190A  
FILING DATE: 26-Aug-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/03918  
FILING DATE: 28-FEB-98  
ATTORNEY/AGENT INFORMATION:  
NAME: MUEPING, ANN M.  
REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 228.00010201  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1228  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 49 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-09-380-190A-37

Query Match 13.0% Score 15.6; DB 4; Length 49;  
Best Local Similarity 63.2%; Pred. No. 7.1e+03;  
Matches 24; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Oy 24 ACCACACCTCATTCCTCCACTCAGAGGAGGATTCAGG 61  
Db 44 ACACATCCACAGGCTCGACCTCCAGTGGATCAAGG 7

RESULT 59  
US-09-255-368-31/c  
Sequence 31, Application US/09255368  
Patent No. 6262246  
GENERAL INFORMATION:  
APPLICANT: Gerald, Christophe P.G.  
APPLICANT: Jones, Kenneth A.  
APPLICANT: Bonini, James A.  
APPLICANT: Borowsky, Beth  
TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors  
FILE REFERENCE: 1795/57155-A  
CURRENT APPLICATION NUMBER: US/09/255.368  
CURRENT FILING DATE: 1999-02-22  
EARLIER APPLICATION NUMBER: 09/161.113  
EARLIER FILING DATE: 1998-09-25  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0 - beta  
SEQ ID NO 31  
LENGTH: 26  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer/probe  
US-09-255-368-31

Query Match 12.8% Score 15.4; DB 4; Length 26;  
Best Local Similarity 76.0%; Pred. No. 6.6e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 16 CCCTCTAACCACCTCATATTC 40  
Db 26 CCCTTTAAACCAAGCTCATATC 2

RESULT 60  
US-08-189-256A-46  
Sequence 46, Application US/08189256A  
Patent No. 58774C2  
GENERAL INFORMATION:  
APPLICANT: Maliga, Pal  
APPLICANT: Svab, Zora  
APPLICANT: Staub, Jeffrey  
APPLICANT: Zoubenko, Oleg V.  
APPLICANT: Allison, Lori A.  
APPLICANT: Carrier, Helaine  
APPLICANT: Kanewski, Ivan  
TITLE OF INVENTION: DNA Constructs and Methods for Stably  
TITLE OF INVENTION: Transforming Plasmids of Multicellular Plants and  
TITLE OF INVENTION: Expressing Recombinant Proteins Therein  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
STREET: 1601 Market Street Suite 720  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103-2307  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/189.256A  
FILING DATE: 31-JAN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/111.398  
FILING DATE: 25-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/518.763  
FILING DATE: 01-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Reed, Janet E.  
REGISTRATION NUMBER: 36,252  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 563-4100  
TELEFAX: (215) 563-4044  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-189-256A-46

Query Match 12.8% Score 15.4; DB 2; Length 33;  
Best Local Similarity 76.0%; Pred. No. 7.2e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 5 TCCCATAGTACCTCTCAACCCAC 29  
Db 9 TTCCATGGTGATCTCTTATTCAC 33

RESULT 61  
US-09-193-853-46  
Sequence 46, Application US/09193853  
Patent No. 6388168  
GENERAL INFORMATION:  
APPLICANT: Maliga, Pal  
APPLICANT: Svab, Zora  
APPLICANT: Staub, Jeffrey  
APPLICANT: Zoubenko, Oleg V.

|||||||    |    |||||    |    |||||    |    |||||    |

1 AACCAATACATGTATTAGTACTGAAAGTGATTCAGAGGGTTACA 46

RESULT 57  
US-08-487-860-34  
Sequence 34, Application US/08487860  
Patent No. 5792456  
GENERAL INFORMATION:  
APPLICANT: Yellon, Dale  
INVENTOR: Glaser, Scott  
APPlicant: Huse, William  
TITLE OF INVENTION: Rosok., Mae J.  
PURPOSE OF INVENTION: Functional Equivalents Reactive With Human Carcinomas  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 1150 Santa Monica Blvd., Suite 400  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90025-3395  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,860  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Adriano, Sarah B.  
REGISTRATION NUMBER: 34,470  
REFERENCE/DOCKET NUMBER: 30436.16U\$01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 310-445-1140  
TELEFAX: 310-445-9031  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-487-860-34

Query Match 13.0% Score 15.6; DB 1: Length 48;  
Best Local Similarity 36.7%; Freq.No./e+03;  
Matches 23 Conservative 0 Mismatches 19 Indels 0 Gaps 0

QY  
AACCACTCATTTATCCCTCGAGGGATTTCAGGGTTCCA 68  
|||||||  
1 AACCAATACATGTATTAGTACTGAAAGTGATTCAGAGGGTTACA 46  
DBD

RFSULLI 58  
US-09-380-190A-37/C  
Sequence 37, Application US/09380190A  
Patent No. 6410220  
GENERAL INFORMATION:  
TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES THEREOF  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MUETTING, RAASCH & GEHARDT, P.A.  
STREET: 119 NORTH FOURTH STREET, SUITE 203  
CITY: MINNEAPOLIS  
STATE: MINNESOTA  
COUNTRY: USA  
ZIP: 55401

RESULT 52  
US-09-387-800-6/c  
Sequence 6, Application US/09387800  
Patent No. 6280972  
GENERAL INFORMATION:  
APPLICANT: YASUDA, Hisashi  
TITLE OF INVENTION: NOVEL ACTIVATOR FOR ALCOHOL DEHYDROGENASE AND GENE  
FILE REFERENCE: 0010-1036-0  
CURRENT APPLICATION NUMBER: US/09/387,800  
EARLIER FILING DATE: 1999-09-01  
EARLIER FILING DATE: 1998-09-02  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 6  
LENGTH: 38  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: BS-YQKG2-2  
US-09-387-800-6

Query Match 13.0% Score 15.6; DB 4; Length 38;  
Best Local Similarity 70.0%; Pred. No. 6.4e+03;  
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 61 GGGTCCAGCGTTCCTCGAATGATCGATT 90  
DB 32 GCGTCCAGCGCGCGCTGAAGGATCCATT 3

RESULT 53  
US-09-463-682-15/c  
Sequence 15, Application US/08463682  
Patent No. 6008193  
GENERAL INFORMATION:  
APPLICANT: Leonard Garfinkel, et al.  
TITLE OF INVENTION: Cloning and Production of Human Von Willebrand Factor GPIIb Binding Domain Polypeptides and Methods of Using Same  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 1185 Avenue of Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/463,682  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 36537-B2-Y  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-463-682-15

Query Match 13.0% Score 15.6; DB 4; Length 38;  
Best Local Similarity 70.0%; Pred. No. 6.4e+03;  
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 61 GGGTCCAGCGTTCCTCGAATGATCGATT 90  
DB 32 GCGTCCAGCGCGCGCTGAAGGATCCATT 3

RESULT 54  
US-08-463-682-13/c  
Sequence 13, Application US/08463682  
Patent No. 6008193  
GENERAL INFORMATION:  
APPLICANT: Leonard Garfinkel, et al.  
TITLE OF INVENTION: Cloning and Production of Human Von Willebrand Factor GPIIb Binding Domain Polypeptides and Methods of Using Same  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 1185 Avenue of Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/463,682  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 36537-B2-Y  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-463-682-13

Query Match 13.0% Score 15.6; DB 3; Length 46;  
Best Local Similarity 70.0%; Pred. No. 6.9e+03;  
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 44 ACTCCAGAGGGATTCCAGGGTCCAGCGTT 73  
DB 42 ACTATAGAAATGAACCCGGGTCGCCAGCTTT 13

RESULT 55  
US-09-173-043-12  
Sequence 12, Application US/09173043  
Patent No. 6207442  
GENERAL INFORMATION:  
APPLICANT: Raymond, Christopher K.  
TITLE OF INVENTION: PLASMID CONSTRUCTION BY HOMOLOGOUS RECOMBINATION

ANTI-SENSE: NO  
US-08-463-682-15

Query Match 13.0% Score 15.6; DB 3; Length 45;  
Best Local Similarity 70.0%; Pred. No. 6.9e+03;  
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 44 ACTCCAGAGGGATTCCAGGGTCCAGCGTT 73  
DB 41 ACTATAGAAATGAACCCGGGTCGCCAGCTTT 12

RESULT 54  
US-08-463-682-13/c  
Sequence 13, Application US/08463682  
Patent No. 6008193  
GENERAL INFORMATION:  
APPLICANT: Leonard Garfinkel, et al.  
TITLE OF INVENTION: Cloning and Production of Human Von Willebrand Factor GPIIb Binding Domain Polypeptides and Methods of Using Same  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 1185 Avenue of Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/463,682  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 36537-B2-Y  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-463-682-13

Query Match 13.0% Score 15.6; DB 3; Length 46;  
Best Local Similarity 70.0%; Pred. No. 6.9e+03;  
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 44 ACTCCAGAGGGATTCCAGGGTCCAGCGTT 73  
DB 42 ACTATAGAAATGAACCCGGGTCGCCAGCTTT 13

RESULT 55  
US-09-173-043-12  
Sequence 12, Application US/09173043  
Patent No. 6207442  
GENERAL INFORMATION:  
APPLICANT: Raymond, Christopher K.  
TITLE OF INVENTION: PLASMID CONSTRUCTION BY HOMOLOGOUS RECOMBINATION



TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
US-08-829-525-29

Query Match 13.0%; Score 15.6; DB 3; Length 31;  
Best Local Similarity 70.0%; Pred. No. 6e+03; 9; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 42 CCATCCAGGAGGATTCAGGGGTTCCAGCG 71  
||||| ||||| ||||| ||||| ||||| |||||  
Db 31 CCACCCAGGAGGATTTACTGTACCCGCG 2

RESULT 47  
US-08-609-583A-29/c  
Sequence 29, Application US/08609583A  
Patent No. 6204371  
GENERAL INFORMATION:  
APPLICANT: Levinson, Douglas A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/609,583A  
FILING DATE: 01-MAR-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,748  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/398,633  
FILING DATE: 03-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 7853-048  
REFERENCE/DOCKET NUMBER: 7853-048  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
US-08-609-583A-29

Query Match 13.0%; Score 15.6; DB 4; Length 31;  
Best Local Similarity 70.0%; Pred. No. 6e+03; 9; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
Oy 42 CCATCCAGGAGGATTCAGGGGTTCCAGCG 71  
||||| ||||| ||||| ||||| ||||| |||||  
Db 31 CCACCCAGGAGGATTTACTGTACCCGCG 2

RESULT 48  
US-08-937-399-29/c  
Sequence 29, Application US/08937399  
Patent No. 6288218  
GENERAL INFORMATION:  
APPLICANT: Levinson, Douglas A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/937,399  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/609,583  
FILING DATE: 01-MAR-1996  
APPLICATION NUMBER: US 08/487,748  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/398,633  
FILING DATE: 03-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-048  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
US-08-937-399-29

Query Match 13.0%; Score 15.6; DB 4; Length 31;  
Best Local Similarity 70.0%; Pred. No. 6e+03; 9; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 42 CCATCCAGGAGGATTCAGGGGTTCCAGCG 71  
||||| ||||| ||||| ||||| ||||| |||||  
Db 31 CCACCCAGGAGGATTTACTGTACCCGCG 2

RESULT 49  
US-08-560-639-24/c  
Sequence 24, Application US/09560639  
Patent No. 6323334  
GENERAL INFORMATION:  
APPLICANT: Kingsbury, G.  
APPLICANT: Leiby, K.

CLASSIFICATION: 514  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,403  
FILING DATE: 28-APR-1994  
APPLICATION NUMBER: US 07/934,375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098,766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454,450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636,662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158,015  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-450-236-36

Query Match 13.0% Score 15.6; DB 1: Length 27;  
Best Local Similarity 81.8%; Pred. No. 5.7e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 3 GATGCCATAGTGCCTCTCTAA 24  
DB 6 GAAGCCATGCTGACTCTCCCA 27

RESULT 45  
US-08-235-403-36  
Sequence 36, Application US/08235403  
Patent No. 6316003  
GENERAL INFORMATION:  
APPLICANT: FRANKEL, Alan  
APPLICANT: PABO, Carl  
APPLICANT: BARSOOM, James G.  
APPLICANT: FAWELL, Stephen E.  
TITLE OF INVENTION: TAG-DERIVED TRANSPORT POLYPEPTIDES  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/235,403  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/934,375

FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098,766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454,450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636,662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158,015  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-235-403-36

Query Match 13.0% Score 15.6; DB 4: Length 27;  
Best Local Similarity 81.8%; Pred. No. 5.7e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 3 GATGCCATAGTGCCTCTCTAA 24  
DB 6 GAAGCCATGCTGACTCTCCCA 27

RESULT 46  
US-08-829-525-29/c  
Sequence 29, Application US/08829525  
Patent No. 6084083  
GENERAL INFORMATION:  
APPLICANT: LEVINSON, Douglas A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM- compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: PatentIn Release Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/829,525  
FILING DATE: 28-MAR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/609,583  
FILING DATE: 01-MAR-1996  
APPLICATION NUMBER: US 08/487,748  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/398,633  
FILING DATE: 03-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-081

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: ZIP: 10020
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/450.098
: FILING DATE: 25-MAY-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/235,403
: FILING DATE: 28-APR-1994
: APPLICATION NUMBER: US 07/934,375
: FILING DATE: 21-AUG-1992
: APPLICATION NUMBER: US 07/098,766
: FILING DATE: 28-JUL-1993
: APPLICATION NUMBER: PCT/US93/07833
: FILING DATE: 19-AUG-1993
: APPLICATION NUMBER: US 07/454,450
: FILING DATE: 21-DEC-1989
: APPLICATION NUMBER: US 07/636,662
: FILING DATE: 02-JAN-1991
: APPLICATION NUMBER: US 07/636,662
: FILING DATE: 02-JAN-1991
: APPLICATION NUMBER: US 08/158,015
: FILING DATE: 24-NOV-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Haley Jr., James F.
: REGISTRATION NUMBER: 27,794
: REFERENCE/DOCKET NUMBER: B170 CIP 2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 596-9000
: TELEFAX: (212) 596-9090
: TELEX: 14-8367
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 27 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-450-098-36

Query Match 13.0% Score 15.6; DB 1; Length 27;
Best Local Similarity 81.8%; Pred. No. 5.7e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GATGCCATAGTACCCCTCTAA 24
Db 6 GAAGCCATGTGCTCTCCCAA 27

RESULT 43
US-08-451-233-36
: Sequence 36, Application US/08451233
: Patent No. 15747641
: GENERAL INFORMATION:
: APPLICANT: FRANKEL, Alan
: APPLICANT: PABO, Carl
: APPLICANT: BARSOUM, James G.
: APPLICANT: FAWELL, Stephen E.
: APPLICANT: PEPINSKY, R. B.
: TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
: NUMBER OF SEQUENCES: 69
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FISH & NEAVE
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10020
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/450.098
: FILING DATE: 25-MAY-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/235,403
: FILING DATE: 28-APR-1994
: APPLICATION NUMBER: US 07/934,375
: FILING DATE: 21-AUG-1992
: APPLICATION NUMBER: US 07/098,766
: FILING DATE: 28-JUL-1993
: APPLICATION NUMBER: PCT/US93/07833
: FILING DATE: 19-AUG-1993
: APPLICATION NUMBER: US 07/454,450
: FILING DATE: 21-DEC-1989
: APPLICATION NUMBER: US 07/636,662
: FILING DATE: 02-JAN-1991
: APPLICATION NUMBER: US 08/158,015
: FILING DATE: 24-NOV-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Haley Jr., James F.
: REGISTRATION NUMBER: 27,794
: REFERENCE/DOCKET NUMBER: B170 CIP 2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 596-9000
: TELEFAX: (212) 596-9090
: TELEX: 14-8367
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 27 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-450-098-36

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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/451.233
: FILING DATE: 25-MAY-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/235,403
: FILING DATE: 28-APR-1994
: APPLICATION NUMBER: US 07/934,375
: FILING DATE: 21-AUG-1992
: APPLICATION NUMBER: US 07/098,766
: FILING DATE: 28-JUL-1993
: APPLICATION NUMBER: PCT/US93/07833
: FILING DATE: 19-AUG-1993
: APPLICATION NUMBER: US 07/454,450
: FILING DATE: 21-DEC-1989
: APPLICATION NUMBER: US 07/636,662
: FILING DATE: 02-JAN-1991
: APPLICATION NUMBER: US 08/158,015
: FILING DATE: 24-NOV-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Haley Jr., James F.
: REGISTRATION NUMBER: 27,794
: REFERENCE/DOCKET NUMBER: B170 CIP 2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 596-9000
: TELEFAX: (212) 596-9090
: TELEX: 14-8367
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 27 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-451-233-36

Query Match 13.0% Score 15.6; DB 1; Length 27;
Best Local Similarity 81.8%; Pred. No. 5.7e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GATGCCATAGTACCCCTCTAA 24
Db 6 GAAGCCATGTGCTCTCCCAA 27

RESULT 44
US-08-450-236-36
: Sequence 36, Application US/08450236
: Patent No. 5804604
: GENERAL INFORMATION:
: APPLICANT: FRANKEL, Alan
: APPLICANT: PABO, Carl
: APPLICANT: BARSOUM, James G.
: APPLICANT: FAWELL, Stephen E.
: APPLICANT: PEPINSKY, R. B.
: TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
: NUMBER OF SEQUENCES: 69
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FISH & NEAVE
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10020
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/450.236

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TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,257  
FILING DATE: 25-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,403  
FILING DATE: 28-APR-1994  
APPLICATION NUMBER: US 07/934,375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098,766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454,450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636,662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158,015  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley J.F. James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-450-257-36  
Query Match 13.0% Score 15.6: DB 1: Length 27:  
Best Local Similarity 81.8% Pred. No. 5.7e-03:  
Matches 18: Conservative 0: Mismatches 4: Indels 0: Gaps 0:  
Oy 3 GATCCATAGTGACCTCTCTAA 24  
Db 6 GAAGCCATGGTGACTCTCCAA 27  
RESULT 41  
US-08-450-246-36  
Sequence 36: Application US/08/50246  
Patent No. 5674980  
GENERAL INFORMATION:  
APPLICANT: FRANKEL, Alan  
APPLICANT: PABO, Carl  
APPLICANT: BARSOOM, James G.  
APPLICANT: FANELL, Stephen E.  
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA

STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,246  
FILING DATE: 25-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/235,403  
FILING DATE: 28-APR-1994  
APPLICATION NUMBER: US 07/934,375  
FILING DATE: 21-AUG-1992  
APPLICATION NUMBER: US 07/098,766  
FILING DATE: 28-JUL-1993  
APPLICATION NUMBER: PCT/US93/07833  
FILING DATE: 19-AUG-1993  
APPLICATION NUMBER: US 07/454,450  
FILING DATE: 21-DEC-1989  
APPLICATION NUMBER: US 07/636,662  
FILING DATE: 02-JAN-1991  
APPLICATION NUMBER: US 08/158,015  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley J.F. James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: B170 CIP 2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-450-246-36  
Query Match 13.0% Score 15.6: DB 1: Length 27:  
Best Local Similarity 81.8% Pred. No. 5.7e-03:  
Matches 18: Conservative 0: Mismatches 4: Indels 0: Gaps 0:  
Oy 3 GATCCATAGTGACCTCTCTAA 24  
Db 6 GAAGCCATGGTGACTCTCCAA 27  
RESULT 42  
US-08-450-098-36  
Sequence 36: Application US/08/450098  
Patent No. 5674980  
GENERAL INFORMATION:  
APPLICANT: FRANKEL, Alan  
APPLICANT: PABO, Carl  
APPLICANT: BARSOOM, James G.  
APPLICANT: FANELL, Stephen E.  
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA



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; EARLIER FILING DATE: 1992-10-29
; EARLIER APPLICATION NUMBER: US 07/603,635
; EARLIER FILING DATE: 1990-10-25
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 5
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: An oligonucleotide
US-08-213-741-6

Query Match      13.5%  Score 16.2; DB 3; Length 45;
Best Local Similarity 64.9%  Pred. No. 4.2e+03;
Matches 24; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Oy 55 ATTGACGGGTTCACACCGCTTCTCGAAATGATCGATTG 91
    ||| | | | | | | | | | | | | | | | | | |
Db 6 ATTAAATAGCTAGCATGATTGACAAAGATGCTTTC 42

RESULT 34
US-08-522-336-6
; Sequence 6, Application US/08522336A
; Patent No. 6287863
; GENERAL INFORMATION:
; APPLICANT: Hodgson, Clague P.
; FILE REFERENCE: 18 08US
; CURRENT APPLICATION NUMBER: US/08/522,336A
; EARLIER FILING DATE: 1995-11-09
; EARLIER APPLICATION NUMBER: PCT/US94/02752
; EARLIER FILING DATE: 1994-03-14
; EARLIER APPLICATION NUMBER: US 08/194,208
; EARLIER FILING DATE: 1994-02-07
; EARLIER APPLICATION NUMBER: US 08/130,638
; EARLIER FILING DATE: 1993-10-01
; EARLIER APPLICATION NUMBER: US 08/097,721
; EARLIER FILING DATE: 1993-07-26
; EARLIER APPLICATION NUMBER: US 08/060,568
; EARLIER FILING DATE: 1993-05-12
; EARLIER APPLICATION NUMBER: US 08/030,766
; EARLIER FILING DATE: 1993-03-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 6
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: An oligonucleotide
US-08-522-336-6

Query Match      13.5%  Score 16.2; DB 4; Length 45;
Best Local Similarity 64.9%  Pred. No. 4.2e+03;
Matches 24; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Oy 55 ATTGACGGGTTCACACCGCTTCTCGAAATGATCGATTG 91
    ||| | | | | | | | | | | | | | | | | | |
Db 6 ATTAAATAGCTAGCATGATTGACAAAGATGCTTTC 42

RESULT 35
US-09-270-140A-71/c
; Sequence 71, Application US/09270140A
; Patent No. 6361941
; GENERAL INFORMATION:
; APPLICANT: Todd, Allison
; APPLICANT: Fuery, Caroline
; APPLICANT: Cairns, Murray
; TITLE OF INVENTION: Catalytic Nucleic Acid base Diagnostic Methods
; FILE REFERENCE: J6J1799
```

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; CURRENT APPLICATION NUMBER: US/09/270,140A
; CURRENT FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 60/079,651
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: RetentIn Ver. 2.1
; SEQ ID NO: 71
; LENGTH: 45
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ribozyme for
; OTHER INFORMATION: codon 215 - mutant (C to U or A)
US-09-270-140A-71

Query Match      13.5%  Score 16.2; DB 4; Length 45;
Best Local Similarity 72.4%  Pred. No. 4.2e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 17 CCTCTCAACCCACCTCATATATCCCCAC 45
    ||| | | | | | | | | | | | | | | | | | |
Db 31 CGTCCTCAGCGGATCATCAGATCCCCAC 3

RESULT 36
PCT-US94-02559-1/c
; Sequence 1, Application PCT/US9402559
; GENERAL INFORMATION:
; APPLICANT: Kamehameha Kay-Min Wong, Jr.
; TITLE OF INVENTION: Ribozymes Which Cleave
; TITLE OF INVENTION: The Transforming Genes of Human
; NUMBER OF SEQ ID NOS: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hoge
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4"
; MEDIUM TYPE: diskette
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS-DOS (R) Version
; OPERATING SYSTEM: 3.30
; SOFTWARE: Microsoft (R)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02559
; FILING DATE: 08 March 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA: None
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: None
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; TELEFAX: None
; INFORMATION FOR SEQ ID NO: 1:
; SOURCE: Characteristic:
; LENGTH: 45
; TYPE: Nucleotide
; STRANDEDNESS: Single
; TOPOLOGY: Linear
PCT-US94-02559-1

Query Match      13.5%  Score 16.2; DB 5; Length 46;
Best Local Similarity 60.0%  Pred. No. 4.2e+03;
Matches 27; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
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US-08-901-379-12/6  
FILING DATE: 27-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Moran, Thomas F  
REGISTRATION NUMBER: 16,579  
REFERENCE/DOCKET NUMBER: 38025-2  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 977-9809  
INFORMATION FOR SEQ ID NO: 12:  
LENGTH: 39 base pairs  
SEQUENCE CHARACTERISTICS:  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..39  
OTHER INFORMATION:  
US-09-234-163-12  
Query Match 13.5% Score 16.2; DB 3; Length 39;  
Best Local Similarity 85.7% Pred. No. 4e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 89 TTGGCTTCCTAGCTCTGAA 109  
Db 35 TTAGCTTCCTAGCTCTGAA 15  
RESULT 28  
US-08-901-379-12/6  
Sequence 12, Application US/08901379  
Patent No. 5879905  
GENERAL INFORMATION:  
APPLICANT: Van Haute, Eddie  
ADDRESS: Ameloot, Paul  
APPLICANT: De Lafontaine, Jean  
APPLICANT: Fiers, Walter  
TITLE OF INVENTION: Genetic Manipulations With Recombinant DNA  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
STREET: 30 Rockefeller Plaza  
CITY: New York, New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/901,379  
FILING DATE: 28-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/147,927  
FILING DATE: 34-NOV-1993  
APPLICATION NUMBER: US 07/592,206  
FILING DATE: 03-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NL 8902452  
FILING DATE: 03-OCT-1985  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NL 9001711  
FILING DATE: 27-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Moran, Thomas F  
REGISTRATION NUMBER: 16,579  
REFERENCE/DOCKET NUMBER: 38025-2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 977-9809  
INFORMATION FOR SEQ ID NO: 12:  
LENGTH: 39 base pairs  
SEQUENCE CHARACTERISTICS:  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..39  
OTHER INFORMATION:  
US-08-901-379-12  
Query Match 13.5% Score 16.2; DB 4; Length 39;  
Best Local Similarity 85.7% Pred. No. 4e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 89 TTGGCTTCCTAGCTCTGAA 109  
Db 35 TTAGCTTCCTAGCTCTGAA 15  
RESULT 29  
US-08-705-196-2/6  
Sequence 2, Application US/08705196  
Patent No. 5879905  
GENERAL INFORMATION:  
APPLICANT: RajBhandary, Ullam L.  
TITLE OF INVENTION: In Vivo Method of Initiating Protein  
SYNTHESIS WITH AN AMINO ACID OTHER THAN METHIONINE  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Hillside Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/705,196  
FILING DATE: 29-AUG-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: MIT-7352  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781) 861-6240  
TELEFAX: (781) 861-9540  
INFORMATION FOR SEQ ID NO: 2:  
LENGTH: 41 base pairs  
SEQUENCE CHARACTERISTICS:  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
US-08-705-196-2  
Query Match 13.5% Score 16.2; DB 2; Length 41;  
Best Local Similarity 85.7% Pred. No. 4e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 89 TTGGCTTCCTAGCTCTGAA 109  
Db 22 TTAGCTTCCTAGCTCTGAA 2

## RESULT 25

PCT-US95-02275-33  
: Sequence 33, Application PC/TUS9502275  
: GENERAL INFORMATION:  
: APPLICANT: Wistar Institute of Anatomy & Biology  
: TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use  
: TITLE OF INVENTION: Thereof  
: NUMBER OF SEQUENCES: 39  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Howson and Howson  
: STREET: Spring House Corporate Cntr, P.O. Box 457  
: CITY: Spring House  
: STATE: Pennsylvania  
: COUNTRY: USA  
: ZIP: 19477  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: PCT/US95/02275  
: FILING DATE:  
: CLASSIFICATION:  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/280,443  
: FILING DATE: 25-JUL-1994  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/197,794  
: FILING DATE: 17-FEB-1994  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Bak, Mary E.  
: REGISTRATION NUMBER: 31,215  
: REFERENCE/DOCKET NUMBER: WST49BPCT  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 215-540-9206  
: TELEFAX: 215-540-5818  
: INFORMATION FOR SEQ ID NO: 33:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 32 base pairs  
: TYPE: 1 nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: unknown  
: MOLECULE TYPE: cDNA  
PCT-US95-02275-33

Query Match 13.5% Score 16.2; DB 5; Length 32;  
Best Local Similarity 70.0%; Pred. No. 3.7e+03;  
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 60 GGGTTCCAGCGTCTCGAATGATCGAT 89  
DB 2 GGGATCCGATCGATCGGGAATGATCGAT 31

## RESULT 26

US-08-961-083-378  
: Sequence 378, Application US/08961083  
: Patent No. 6159469  
: GENERAL INFORMATION:  
: APPLICANT: Choi et. al.  
: TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
: NUMBER OF SEQUENCES: 452  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Human Genome Sciences, Inc.  
: STREET: 9410 Key West Avenue  
: CITY: Rockville  
: STATE: Maryland  
: COUNTRY: USA  
: ZIP: 20850  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
: COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII text  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/961.083  
: FILING DATE:  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER:  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Brookes, A. Anders  
: REGISTRATION NUMBER: 36,373  
: REFERENCE/DOCKET NUMBER: PB340P2  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (301) 309-8504  
: TELEFAX: (301) 309-8512  
: INFORMATION FOR SEQ ID NO: 378:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 37 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: linear  
US-08-961-083-378

Query Match 13.5% Score 16.2; DB 3; Length 37;  
Best Local Similarity 72.4%; Pred. No. 3.9e+03;  
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 11 AGTGACCTCTTACCCACACCTCATTTAT 39  
DB 2 AGTAAGCTTCGGAACCAATTCGCCATTAT 30

## RESULT 27

US-09-234-163-12/c  
: Sequence 12, Application US/09234163  
: Patent No. 6093554  
: GENERAL INFORMATION:  
: APPLICANT: Van Haute, Eddie  
: APPLICANT: Ameloot, Paul  
: APPLICANT: De Lafontaine, Jean  
: APPLICANT: Fiers, Walter  
: TITLE OF INVENTION: Genetic Manipulations With Recombinant DNA  
: TITLE OF INVENTION: Comprising Sequences Derived From RNA Virus  
: NUMBER OF SEQUENCES: 13  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Cooper & Dunham  
: STREET: 30 Rockefeller Plaza  
: CITY: New York, New York  
: STATE: New York  
: COUNTRY: USA  
: ZIP: 10112  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.24  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/234,163  
: FILING DATE:  
: CLASSIFICATION:  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US/08/901,379  
: FILING DATE: 28-JUL-1997  
: APPLICATION NUMBER: 08/147,927  
: FILING DATE: 04-NOV-1993  
: APPLICATION NUMBER: US 07/592,206  
: FILING DATE: 03-OCT-1990  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: NL 8902452  
: FILING DATE: 03-OCT-1989  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: NL 9001711



NAME: Kurt G. Briscoe  
REGISTRATION NUMBER: 33,141  
REFERENCE/DOCKET NUMBER: C0PLO-556-KGB  
TELEPHONE: (914) 332-1700  
TELEFAX: (914) 332-1844  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 Nucleotides  
TYPE: Nucleotide  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
US-08-753-054-12

Query Match 13.7% Score 15.4; DB 1; Length 42;  
Best Local Similarity 50.0%; Pred. No. 3.4e+03;  
Matches 20; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 31 CCTCATTTCCCACTCCAGAGGATTTCAGGGTTCCAGC 70  
DB 41 CCCCATTTTCGTCGCCMCGTGACTSGRAYCCAGC 2

RESULT 20  
US-08-607-269-11  
Sequence 11; Application US/08607269  
Patent No. 5702897  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Sato, Takaaki  
TITLE OF INVENTION: Interaction of Proteins Involved in a  
TITLE OF INVENTION: Cell Death Pathway  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/607,269  
FILING DATE: 13-APR-1994  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/226,876  
FILING DATE: 13-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9882  
TELEPHONE: (619) 535-8949  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-607-269-11

Query Match 13.5% Score 16.2; DB 1; Length 25;  
Best Local Similarity 85.7%; Pred. No. 3.3e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 57 TCAGCGGTTCCAGGTTCTCTG 77  
DB 57 TCAGCGGTTCCAGGTTCTCTG 77

DB 5 TCAGCGGTTGAGCGTTCTCTG 25

## RESULT 21

PCT-US95-04600-11  
Sequence 11; Application PC/TUS9504600  
GENERAL INFORMATION:  
APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION  
TITLE OF INVENTION: Interaction of Proteins Involved in  
TITLE OF INVENTION: a Cell Death Pathway  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04600  
FILING DATE: 12-APR-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Imbra, Richard J.  
REGISTRATION NUMBER: 37,643  
REFERENCE/DOCKET NUMBER: FP-LJ 1361  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US95-04600-11

Query Match 13.5% Score 16.2; DB 5; Length 25;  
Best Local Similarity 85.7%; Pred. No. 3.3e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 57 TCAGCGGTTCCAGGTTCTCTG 77  
DB 5 TCAGCGGTTGAGCGTTCTCTG 25

## RESULT 22

US-08-280-443-33  
Sequence 33; Application US/08280443  
Patent No. 5643778  
GENERAL INFORMATION:  
APPLICANT: Nishikura, Kazuko  
TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr, P.O. Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:





PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brooks, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB340P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 323:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-961-083-323

Query Match 14.08: Score 16.6; DB 3: Length 31;  
Best Local Similarity 75.08; Pred. No. 2.2e+03;  
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 71 GTTCTGAAATGATGCGATTGGCTTCCA 98  
Db 31 GTTCTGAAAGTGAAGTCTTTGGGATCCA 4

RESULT 14  
US-08-389-812-2/c  
Sequence 2, Application US/08389812  
Patent No. 6015665  
GENERAL INFORMATION:  
APPLICANT: DIXIT, VISHVA M.  
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REGULATING  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/389,812  
FILING DATE: 13-FEB-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: KOSKI, ANTOINETTE F.  
REGISTRATION NUMBER: 34,202  
REFERENCE/DOCKET NUMBER: UM 1036.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 856-2400  
TELEFAX: (650) 856-9299  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-270-813-2

Query Match 13.84: Score 16.6; DB 3: Length 40;  
Best Local Similarity 64.18; Pred. No. 2.9e+03;  
Matches 25; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 14 GACCTCTTCAACCCACCTCATTTATCCCACTCCAGAG 52  
Db 40 GATATTGCTCTCCAACTAATTAACCTCGAGTCTAGAG 2

RESULT 16  
US-08-591-605-9/c  
Sequence 9, Application US/08591605  
Patent No. 6060218  
GENERAL INFORMATION:  
APPLICANT: DIXIT, VISHVA M.  
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REGULATING  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-424-663-1

Query Match 14.2% Score 17; DB 1; Length 37;  
Best Local Similarity 69.7%; Pred. No. 2e+03;  
Matches 23; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 16 CCTCTCAACCCACACCTCATTCCTCCACTCC 48  
DB 2 CTCCTCCCTCCCTCTCTCTCTCTCTCTCTCTCC 34

RESULT 11  
US-08-872-446-1  
Sequence 1, Application US/08872446

Patent No. 5569119  
GENERAL INFORMATION:  
APPLICANT: Macevicz, Stephen C.  
TITLE OF INVENTION: DNA Sequencing by Parallel  
TITLE OF INVENTION: Oligonucleotide Extensions  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/872,446  
FILING DATE: 17-APR-1995

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/424,663  
FILING DATE: 17-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Powers, Vincent M.  
REGISTRATION NUMBER: 36,246  
REFERENCE/DOCKET NUMBER: 5525-0015/peolus  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 324-0960  
TELEFAX: (650) 324-0960  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-872-446-1

Query Match 14.2% Score 17; DB 2; Length 37;  
Best Local Similarity 69.7%; Pred. No. 2e+03;  
Matches 23; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 16 CCTCTCAACCCACACCTCATTCCTCCACTCC 48  
DB 2 CTCCTCCCTCCCTCTCTCTCTCTCTCTCTCTCC 34

RESULT 12  
US-09-280-270A-1  
Sequence 1, Application US/09280270A  
Patent No. 6306597

GENERAL INFORMATION:  
APPLICANT: Macevicz, Stephen C.  
TITLE OF INVENTION: DNA Sequencing by Parallel  
TITLE OF INVENTION: Oligonucleotide Extensions  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/280,270A  
FILING DATE: 25-Mar-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/424,663  
FILING DATE: 17-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Powers, Vincent M.  
REGISTRATION NUMBER: 36,246  
REFERENCE/DOCKET NUMBER: 5525-0015/peolus

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 324-0880  
TELEFAX: (650) 324-0960  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-280-270A-1

Query Match 14.2% Score 17; DB 4; Length 37;  
Best Local Similarity 69.7%; Pred. No. 2e+03;  
Matches 23; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 16 CCTCTCAACCCACACCTCATTCCTCCACTCC 48  
DB 2 CTCCTCCCTCCCTCTCTCTCTCTCTCTCTCTCC 34

RESULT 13  
US-08-961-083-323/C  
Sequence 323, Application US/08961083  
Patent No. 6159469  
GENERAL INFORMATION:  
APPLICANT: Choi et. al.  
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
NUMBER OF SEQUENCES: 452  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,083  
FILING DATE:  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/155,005  
FILING DATE: 10-FEBRUARY-1994  
CLASSIFICATION: 536  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX07/D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 145:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: All C's are 2'-NH2 cytosine  
FEATURE:  
OTHER INFORMATION: All U's are 2'-NH2 uracil  
US-08-384-708A-145

Query Match 14.2% Score 17: DB 1: Length 30:  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CCCTCCTAACCCACACC 32  
Db 29 CCCTCCTAACCCACACC 13

## RESULT 9

US-08-687-421-145/C  
Sequence 145: Application US/08687421  
Patent No. 5177557  
GENERAL INFORMATION:  
APPLICANT: Gold, Larry  
APPLICANT: Janjic, Nebojsa  
APPLICANT: Tasset, Diane  
TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC  
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND  
TITLE OF INVENTION: THROMBIN  
NUMBER OF SEQUENCES: 445  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C. 200  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER/READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/687,421  
FILING DATE: 08-MAY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/195,005  
FILING DATE: 10-FEBRUARY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE: 22-APRIL-1993  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/219,012  
FILING DATE: 28-MARCH-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/973,333  
FILING DATE: 11-NOVEMBER-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX07/PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 145:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: All C's are 2'-NH2 cytosine  
FEATURE:  
OTHER INFORMATION: All U's are 2'-NH2 uracil  
US-08-687-421-145

Query Match 14.2% Score 17: DB 4: Length 30:  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CCCTCCTAACCCACACC 32  
Db 29 CCCTCCTAACCCACACC 13

## RESULT 10

US-08-663-1  
Sequence 1: Application US/08424663  
Patent No. 5750341  
GENERAL INFORMATION:  
APPLICANT: MACEVICZ, Stephen C.  
TITLE OF INVENTION: DNA Sequencing by Stepwise Extension with Oligonucleotide B  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen C. Macevicz  
STREET: 21890 Rucker Drive  
CITY: Cupertino  
STATE: California  
COUNTRY: USA  
ZIP: 95014  
COMPUTER/READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 3.1/DOS 5.0  
SOFTWARE: Microsoft Word for Windows, vers. 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,663  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Stephen C. Macevicz  
REGISTRATION NUMBER: 30,285  
REFERENCE/DOCKET NUMBER: peo1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 638-5552  
TELEFAX:

```

: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Primer
US-09-383-143-25

Query Match      14 38: Score 17.2: DB 4: Length 37:
Best Local Similarity 86.4%: Pred. No. 1.8e+03:
Matches 25: Conservative 0: Mismatches 13: Indels 0: Gaps 0:

Oy 89 TTGGTTCATAGCTCTCAAT 110
Db 32 TTAGCTCTTAGCTCTCAAT 11

RESULT 6
US-08-872-446-9/C
: Sequence 9: Application US/08872446
: Patent No. 5969119
: GENERAL INFORMATION:
: APPLICANT: Macevicz, Stephen C.
: TITLE OF INVENTION: DNA Sequencing by Parallel
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dehlinger & Associates
: STREET: 350 Cambridge Avenue, Suite 250
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: FILING DATE: 17-Apr-1995
: APPLICATION NUMBER: US/08/872.446
: PRIORITY INFORMATION:
: APPLICATION NUMBER: US 08/424,663
: FILING DATE: 17-Apr-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Powers, Vincent M.
: REGISTRATION NUMBER: 36,246
: REFERENCE/DOCKET NUMBER: 5525-0015/peolus
: TELEPHONE: (650) 324-0960
: TELEFAX: (650) 324-0960
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 45 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-676-436-3

Query Match      14 38: Score 17.2: DB 2: Length 45:
Best Local Similarity 65.8%: Pred. No. 1.8e+03:
Matches 25: Conservative 0: Mismatches 13: Indels 0: Gaps 0:

Oy 11 AGTCACCTCTTACCCACACCTCATATATCCCACTCC 48
Db 45 AGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 8

RESULT 7
US-09-280-270A-9/C
: Sequence 9: Application US/09280270A
: Patent No. 6305597
: GENERAL INFORMATION:
: APPLICANT: Macevicz, Stephen C.
: TITLE OF INVENTION: DNA Sequencing by Parallel
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dehlinger & Associates
: STREET: 350 Cambridge Avenue, Suite 250
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: FILING DATE: 17-Apr-1995
: APPLICATION NUMBER: US/08/872.446
: PRIORITY INFORMATION:
: APPLICATION NUMBER: US 08/424,663
: FILING DATE: 17-Apr-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Powers, Vincent M.
: REGISTRATION NUMBER: 36,246
: REFERENCE/DOCKET NUMBER: 5525-0015/peolus
: TELEPHONE: (650) 324-0960
: TELEFAX: (650) 324-0960
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 45 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-872-446-9

Query Match      14 38: Score 17.2: DB 2: Length 45:
Best Local Similarity 65.8%: Pred. No. 1.8e+03:
Matches 25: Conservative 0: Mismatches 13: Indels 0: Gaps 0:

Oy 11 AGTCACCTCTTACCCACACCTCATATATCCCACTCC 48
Db 45 AGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 8

RESULT 8
US-08-384-708A-145/C
: Sequence 145: Application US/08384708A
: Patent No. 5639868
: GENERAL INFORMATION:
: APPLICANT: Gold, Larry
: APPLICANT: Janjic, Nobolisa
: TITLE OF INVENTION: High-Affinity RNA Ligands of Basic
: NUMBER OF SEQUENCES: 227
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Swanson & Bratschun, L.L.C.
: STREET: 8400 E. Prentice Avenue, Suite 200
: CITY: Englewood
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage
: COMPUTER: IBM compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WordPerfect 5.1
: CURRENT APPLICATION DATA:
: FILING DATE: 02 FEBRUARY 1995
: CLASSIFICATION: 536
```

CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Fastseq Version 2.0b  
CURRENT APPLICATION NUMBER:  
APPLIC FILING DATE: US/09/638,202A  
FILING DATE: 11-Aug-2000  
PRIOR APPLICATION DATA:  
APPLIC FILING DATE: 09/096,749  
ATTORNEY/AGENT INFORMATION:  
NAME: Ann S. Viskind  
REGISTRATION NUMBER: 37,748  
REFERENCE/DOCKET NUMBER: 109,034051  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (612) 373-6900  
TELEFAX: (612) 339-3061  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-638-202A-23

Query Match 14.8%; Score 17.8; DB 4; Length 38;  
Best Local Similarity 67.6%; Pred. No. 1e+03;  
Matches 25; Conservative 0; Mismatches 12; Indels

**QY** 52 GGGATTCAGGGGTTCCAGCGTCTCCTGAARATGATCGA 80  
||||| || | | | | | | | | | |  
**db** 2 GGATCCACCGGTGCCACCGTAGCTTAATCGA 38

RESULT 3  
US-08-683-743-9/c  
: Sequence 9: Application US/08683743  
: Patent No. 15843697  
: GENERAL INFORMATION:  
: APPLICANT: Pestka, Sidney  
: APPLICANT: Kotenko, Sergei  
: TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION  
: TITLE OF INVENTION: CHAIN  
: NUMBER OF SEQUENCES: 25  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: David A. Jackson, Esq.  
: STREET: 411 Hackensack Ave, Continental Plaza, 4th  
: CITY: Floor  
: STATE: New Jersey  
: COUNTRY: USA  
: ZIP: 07601  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC Compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/683,743  
: FILING DATE: 17-JUL-1996  
: CLASSIFICATION: 435  
: ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 601-1-050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "Oligonucleotides"  
HYPOTHETICAL: NO  
US-08-683-743-9

```
Query Match      14.8%; Score 17.8; DB 2; Length 44;
Best Local Similarity 67.6%; Pred. No. 1.1e+03;
Matches 25; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

**QY**           84 ATCGATTGGCTTCCATAGCTGCTGAATTGCAGTTTAG 120  
               | | | | |  
**DB**           42 AACAACTGGAATCCAAAGTTGTGAAGTCACGTGGAG 6

```

RESULT 4
US-09-383-143-33/c
: Sequence 33, Application US/09383143
: Patent No. 6372429
: GENERAL INFORMATION:
: APPLICANT: SHARON, GIL
: TITLE OF INVENTION: METHOD FOR ASSEMBLY OF MULTIPLE DNA FRAGMENTS
: FILE REFERENCE: LUZZATTO 3.3-061 CONT
: CURRENT APPLICATION NUMBER: US/09/383.143
: CURRENT FILING DATE: 1999-08-25
: PRIOR APPLICATION NUMBER: PCT/IL98/00096
: PRIOR FILING DATE: 1998-02-26
: NUMBER OF SEQ ID NOS: 50
: SOFTWARE: PatentIn ver. 2.1
: SEQ ID NO 33
: LENGTH: 35
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: US-09-383-143-33
: OTHER INFORMATION: Description of Artificial Sequence: Primer

```

Query Match 14.3%; Score 17.2; DB 4; Length 35;  
Best Local Similarity 73.3%; Pred. NO. 1.7e+03;  
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 89 TTGGCTTCCATAGCTAGCTGAATTCAGTTT 118  
 || ||||| ||||| || || ||  
 Db 31 TTAGCTTCTTAGCTCCTGATTCATGTT 2

```

RESULT 5
US-09-383-143-25/c
; Sequence 25, Application US/09383143
; Patent NO. 6372429
; GENERAL INFORMATION:
; APPLICANT: SHARON, GIL
; TITLE OF INVENTION: METHOD FOR ASSEMBLY OF MULTIPLE DNA FRAGMENTS
; FILE REFERENCE: LU22ATTO 3-061 CONT
; CURRENT APPLICATION NUMBER: US/09/383.143
; CURRENT FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/IL98/00096
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 37

```







PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423

SEQ ID NO 16  
LENGTH: 50  
TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: oligonucleotide probe

US-09-907-979-16

Query Match 13.0%; Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8%; Pred. No. 2.7e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Caps 0;

OY 86 CGATTGGCTTCCATAGCTGCTG 107  
||||| || ||||| ||||| |||||  
DB 29 CGATCGATGCCACAGCTGCTG 8

## RESULT 100

US-09-902-615-16/c

Sequence 16, Application US/0902615

PUBLICATION NO. US2003092002A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Peststein, David

APPLICANT: Pestoyers, Luc

APPLICANT: Eston, David L.

APPLICANT: Feltz, William J.

APPLICANT: Feltz, William J.

APPLICANT: Fong, Sherman

APPLICANT: Geo, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerltzen, Mary E.

APPLICANT: Goddard, A. Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavon, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/902.615

CURRENT FILING DATE: 2001-12-14

Prior application data removed. Check file wrapper or PALM.

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 16

LENGTH: 50

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: oligonucleotide probe

US-09-902-615-16

Query Match 13.0%; Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8%; Pred. No. 2.7e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Caps 0;

OY 86 CGATTGGCTTCCATAGCTGCTG 107  
||||| || ||||| ||||| |||||  
DB 29 CGATCGATGCCACAGCTGCTG 8

Search completed: June 17, 2003, 22:50:38  
Job time : 125 secs

## GENERAL INFORMATION:

APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.

## TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/302,713

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 09/665,350

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/30999

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US00/00219

PRIOR FILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 16

LENGTH: 50

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-302-713-16

Query Match 13.0%; Score 15.6; DB 9; Length 50;

Best Local Similarity 81.8%; Pred. No. 2.7e+04;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 86 CGATGGCTTCATAGCTGCTG 107

DB 29 CGATGGATGCCACAGCTGCTG 8

## RESULT 99

US-09-307-979-16/C

Sequence 16, Application US/09907979

Publication No. US20030082542A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/307,979

CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02

## RESULT 96

US-09-905-075-16/c  
; Sequence 16, Application US/0905075  
; Publication No. US20030077583A1

## GENERAL INFORMATION:

APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavib, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: US/09/905,075  
PRIOR FILING DATE: 2001-07-13  
Check file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 16  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Oligonucleotide probe

US-09-905-075-16  
Query Match 13.0%; Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8%; Pred. No. 2.7e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 86 CGATGGCTTCATAGCTGCTG 107  
Db 29 CGATCGATGCCACAGCTGCTG 8

## RESULT 97

US-09-902-634-16/c  
; Sequence 16, Application US/0902634  
; Publication No. US20030082540A1

## GENERAL INFORMATION:

APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavib, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: US/09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-11  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 16  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide Probe

US-09-902-634-16  
Query Match 13.0%; Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8%; Pred. No. 2.7e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 86 CGATGGCTTCATAGCTGCTG 107  
Db 29 CGATCGATGCCACAGCTGCTG 8

## RESULT 98

US-09-902-713-16/c  
; Sequence 16, Application US/0902713  
; Publication No. US20030082541A1

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ;; FILE REFERENCE: 10466-14  
 ;; CURRENT FILING DATE: 2001-12-18  
 ;; PRIOR APPLICATION NUMBER: US/09/907/575  
 ;; PRIOR FILING DATE: 2000-02-22  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ;; PRIOR FILING DATE: 2000-02-22  
 ;; PRIOR APPLICATION NUMBER: US 60/143,048  
 ;; PRIOR FILING DATE: 1999-07-07  
 ;; PRIOR APPLICATION NUMBER: US 60/145,698  
 ;; PRIOR FILING DATE: 1999-07-26  
 ;; PRIOR APPLICATION NUMBER: US 60/146,222  
 ;; PRIOR FILING DATE: 1999-07-26  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/20594  
 ;; PRIOR FILING DATE: 1999-09-08  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/20944  
 ;; PRIOR FILING DATE: 1999-09-13  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ;; PRIOR FILING DATE: 1999-09-15  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/21547  
 ;; PRIOR FILING DATE: 1999-09-15  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/23089  
 ;; PRIOR FILING DATE: 1999-10-05  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/28214  
 ;; PRIOR FILING DATE: 1999-11-29  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
 ;; PRIOR FILING DATE: 1999-11-30  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/28564  
 ;; PRIOR FILING DATE: 1999-12-02  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/28565  
 ;; PRIOR FILING DATE: 1999-12-02  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
 ;; PRIOR FILING DATE: 1999-12-16  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/30911  
 ;; PRIOR FILING DATE: 1999-12-20  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/30999  
 ;; PRIOR FILING DATE: 1999-12-20  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/00219  
 ;; NUMBER OF SEQ ID NOS: 423  
 ;; SEQ ID NO 16  
 ;; LENGTH: 50  
 ;; TYPE: DNA  
 ;; ORGANISM: Artificial Sequence  
 ;; FEATURE:  
 ;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ;; OTHER INFORMATION: oligonucleotide probe

US-09-907-575-16  
 Query Match 13.0%; Score 15.6; DB 9; Length 50;  
 Best Local Similarity 81.8%; Pred. No. 2.7e+04;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 86 CGATGGCTTCCATAGCTGCTG 107  
 Db 29 CGATCGATGCCACAGCTGCTG 8

RESULT 95  
 US-09-902-759-16/c  
 Sequence 16, Application US/09/902/759  
 Publication NO. US20030077654A1

GENERAL INFORMATION:  
 APPLICANT: Genentech, Inc.  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter

;; APPLICANT: Gerritsen, Mary E.  
 ;; APPLICANT: Goddard, A  
 ;; APPLICANT: Godowski, Paul J.  
 ;; APPLICANT: Grimaldi, Christopher J.  
 ;; APPLICANT: Gurney, Austin L.  
 ;; APPLICANT: Hillan, Kenneth, J.  
 ;; APPLICANT: Kijavlin, Ivar J.  
 ;; APPLICANT: Mather, Jennie P.  
 ;; APPLICANT: Pan, James  
 ;; APPLICANT: Paoni, Nicholas F.  
 ;; APPLICANT: Roy, Margaret Ann  
 ;; APPLICANT: Stewart, Timothy A.  
 ;; APPLICANT: Tumas, Daniel  
 ;; APPLICANT: Williams, P. Mickey  
 ;; APPLICANT: Wood, William I.  
 ;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ;; FILE REFERENCE: 10466-14  
 ;; CURRENT FILING DATE: 2001-07-10  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ;; PRIOR FILING DATE: 2000-02-22  
 ;; PRIOR APPLICATION NUMBER: US 60/143,048  
 ;; PRIOR FILING DATE: 1999-07-07  
 ;; PRIOR APPLICATION NUMBER: US 60/145,698  
 ;; PRIOR FILING DATE: 1999-07-26  
 ;; PRIOR APPLICATION NUMBER: US 60/146,222  
 ;; PRIOR FILING DATE: 1999-07-28  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/20594  
 ;; PRIOR FILING DATE: 1999-09-08  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/20944  
 ;; PRIOR FILING DATE: 1999-09-13  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ;; PRIOR FILING DATE: 1999-09-15  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/21547  
 ;; PRIOR FILING DATE: 1999-09-15  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/23089  
 ;; PRIOR FILING DATE: 1999-10-05  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/28214  
 ;; PRIOR FILING DATE: 1999-11-29  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
 ;; PRIOR FILING DATE: 1999-11-30  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/28564  
 ;; PRIOR FILING DATE: 1999-12-02  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/28565  
 ;; PRIOR FILING DATE: 1999-12-02  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
 ;; PRIOR FILING DATE: 1999-12-16  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/30911  
 ;; PRIOR FILING DATE: 1999-12-20  
 ;; PRIOR APPLICATION NUMBER: PCT/US99/30999  
 ;; PRIOR FILING DATE: 1999-12-20  
 ;; PRIOR APPLICATION NUMBER: PCT/US00/00219  
 ;; NUMBER OF SEQ ID NOS: 423  
 ;; SEQ ID NO 16  
 ;; LENGTH: 50  
 ;; TYPE: DNA  
 ;; ORGANISM: Artificial Sequence  
 ;; FEATURE:  
 ;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ;; OTHER INFORMATION: oligonucleotide probe

US-09-902-759-16  
 Query Match 13.0%; Score 15.6; DB 9; Length 50;  
 Best Local Similarity 81.8%; Pred. No. 2.7e+04;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 86 CGATGGCTTCCATAGCTGCTG 107  
 Db 29 CGATCGATGCCACAGCTGCTG 8

```

: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/00219
: PRIOR FILING DATE: 2000-01-05
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 16
: LENGTH: 50
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: Oligonucleotide probe
US-09-905-084-16

Query Match      13.0%  Score 15.6: DB 9; Length 50;
Best Local Similarity 81.8%  Pred No. 2.7e+04;
Matches 18: Conservative 0; Mismatches 4; Indels 0; Gaps 0:

OY      86 CGATGGCTTCACATGCTGCTG 107
Db      29 CGATCGATCCACACGCTGCTG 8

RESULT 93
US-09-905-088-16/c
: Sequence 15, Application US/0905088
: Publication No. US20030073079A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Grifftsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kijavich, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/905-088
: PRIOR FILING DATE: 2001-07-12
: PRIOR APPLICATION NUMBER: 09/665,350
: PRIOR FILING DATE: 2000-09-18
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR FILING DATE: 1999-07-07
: PRIOR FILING DATE: 1999-07-07
: PRIOR FILING DATE: 1999-07-07
: PRIOR FILING DATE: 1999-07-26
: PRIOR FILING DATE: 1999-07-26
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR APPLICATION NUMBER: PCT/US99/20594

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: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/28565
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/00219
: PRIOR FILING DATE: 2000-01-05
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 16
: LENGTH: 50
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-905-088-16

Query Match      13.0%  Score 15.6: DB 9; Length 50;
Best Local Similarity 81.8%  Pred No. 2.7e+04;
Matches 18: Conservative 0; Mismatches 4; Indels 0; Gaps 0:

OY      86 CGATGGCTTCACATGCTGCTG 107
Db      29 CGATCGATCCACACGCTGCTG 8

RESULT 94
US-09-907-575-16/c
: Sequence 16, Application US/0907575
: Publication No. US20030073079A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Grifftsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kijavich, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.

```

GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Paoni, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunes, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/905/381  
PRIOR FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 16  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-905-381-16  
Query Match 13.0%; Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8%; Pred. NO. 2.7e-04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 86 CGATTGCTTCCATAGCTGCTG 107  
||||| ||||| ||||| |||||  
Db 29 CGATCGATGCCACAGCTGCTG 8  
RESULT 92  
US-09-909-084-16/c  
Sequence 16, Application US/09909084  
Publication No. US2003005972A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Paoni, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunes, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/909,064  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 16  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:



THE UNIVERSITY OF CHICAGO



```

1 APPLICANT: Eaton, Dan L.
2 APPLICANT: Ferrara, Napoleone
3 APPLICANT: Filvaroff, Ellen
4 APPLICANT: Fong, Sherman
5 APPLICANT: Gao, Wei-Qiang
6 APPLICANT: Gerber, Hanspeter
7 APPLICANT: Gerritsen, Mary E.
8 APPLICANT: Goddard, A.
9 APPLICANT: Godowski, Paul J.
10 APPLICANT: Grimaldi, Christopher J.
11 APPLICANT: Gurney, Austin L.
12 APPLICANT: Hillan, Kenneth, J.
13 APPLICANT: Kijavini, Ivar J.
14 APPLICANT: Mather, Jennie P.
15 APPLICANT: Pan, James
16 APPLICANT: Peoni, Nicholas F.
17 APPLICANT: Roy, Margaret Ann
18 APPLICANT: Stewart, Timothy A.
19 APPLICANT: Tumas, Daniel
20 APPLICANT: Williams, P. Mickey
21 APPLICANT: Wood, William I.
22 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
23 TITLE OF INVENTION: Acids Encoding the Same
24 FILE REFERENCE: 10466-14
25 CURRENT APPLICATION NUMBER: US/09/903,943
26 PRIOR FILING DATE: 2001-07-11
27 PRIOR APPLICATION NUMBER: 09/665,350
28 PRIOR FILING DATE: 2000-09-18
29 PRIOR APPLICATION NUMBER: PCT/US00/04414
30 PRIOR FILING DATE: 2000-02-22
31 PRIOR APPLICATION NUMBER: US 60/143,048
32 PRIOR FILING DATE: 1999-07-07
33 PRIOR APPLICATION NUMBER: US 60/145,698
34 PRIOR FILING DATE: 1999-07-26
35 PRIOR APPLICATION NUMBER: US 60/146,222
36 PRIOR FILING DATE: 1999-07-28
37 PRIOR APPLICATION NUMBER: PCT/US99/20594
38 PRIOR FILING DATE: 1999-09-13
39 PRIOR APPLICATION NUMBER: PCT/US99/20944
40 PRIOR FILING DATE: 1999-09-15
41 PRIOR APPLICATION NUMBER: PCT/US99/21090
42 PRIOR FILING DATE: 1999-09-15
43 PRIOR APPLICATION NUMBER: PCT/US99/21547
44 PRIOR FILING DATE: 1999-10-05
45 PRIOR APPLICATION NUMBER: PCT/US99/23089
46 PRIOR FILING DATE: 1999-11-29
47 PRIOR APPLICATION NUMBER: PCT/US99/28214
48 PRIOR FILING DATE: 1999-11-30
49 PRIOR APPLICATION NUMBER: PCT/US99/28313
50 PRIOR FILING DATE: 1999-11-30
51 PRIOR APPLICATION NUMBER: PCT/US99/28564
52 PRIOR FILING DATE: 1999-12-02
53 PRIOR APPLICATION NUMBER: PCT/US99/28565
54 PRIOR FILING DATE: 1999-12-02
55 PRIOR APPLICATION NUMBER: PCT/US99/30095
56 PRIOR FILING DATE: 1999-12-16
57 PRIOR APPLICATION NUMBER: PCT/US00/00219
58 PRIOR FILING DATE: 2000-01-05
59 NUMBER OF SEQ ID NOS: 423
60 SEQ ID NO 16
61 LENGTH: 30
62 TYPE: DNA
63 ORGANISM: Artificial Sequence
64 FEATURE:
65 OTHER INFORMATION: Synthetic Oligonucleotide Probe
66 US-09-903-943-16

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Query Match 13.0% Score 15.6; DB 9; Length 50;  
 Best Local Similarity 81.8%; Pred. No. 2.7e+04;

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Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 86 CGATTGGCTTCATAGCTGCTG 107
      ||||| | | | | | | | | | |
Db 29 CGATCGCATCCACAGCTGCTG 8

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RESULT 87  
 US-09-904-462-16/C  
 : Sequence 16, Application US/0904462  
 : GENERAL INFORMATION: US2003005435A1  
 : GENERAL INFORMATION: GENENTECH, INC.  
 : APPLICANT: Genentech, Inc.  
 : APPLICANT: Anikozaki, Avi  
 : APPLICANT: Bolstein, David  
 : APPLICANT: Desnoyers, Luc  
 : APPLICANT: Eaton, Dan L.  
 : APPLICANT: Ferrara, Napoleone  
 : APPLICANT: Filvaroff, Ellen  
 : APPLICANT: Fong, Sherman  
 : APPLICANT: Gao, Wei-Qiang  
 : APPLICANT: Gerber, Hanspeter  
 : APPLICANT: Gerritsen, Mary E.  
 : APPLICANT: Goddard, A.  
 : APPLICANT: Godowski, Paul J.  
 : APPLICANT: Grimaldi, Christopher J.  
 : APPLICANT: Gurney, Austin L.  
 : APPLICANT: Hillan, Kenneth, J.  
 : APPLICANT: Kijavini, Ivar J.  
 : APPLICANT: Mather, Jennie P.  
 : APPLICANT: Pan, James  
 : APPLICANT: Peoni, Nicholas F.  
 : APPLICANT: Roy, Margaret Ann  
 : APPLICANT: Stewart, Timothy A.  
 : APPLICANT: Tumas, Daniel  
 : APPLICANT: Williams, P. Mickey  
 : APPLICANT: Wood, William I.  
 : TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 : TITLE OF INVENTION: Acids Encoding the Same  
 : FILE REFERENCE: 10466-14  
 : CURRENT APPLICATION NUMBER: US/09/904,462  
 : PRIOR FILING DATE: 2001-07-11  
 : PRIOR APPLICATION NUMBER: 09/665,350  
 : PRIOR FILING DATE: 2000-09-18  
 : PRIOR APPLICATION NUMBER: PCT/US00/04414  
 : PRIOR FILING DATE: 2000-02-22  
 : PRIOR APPLICATION NUMBER: US 60/143,048  
 : PRIOR FILING DATE: 1999-07-07  
 : PRIOR APPLICATION NUMBER: US 60/145,698  
 : PRIOR FILING DATE: 1999-07-26  
 : PRIOR APPLICATION NUMBER: US 60/146,222  
 : PRIOR FILING DATE: 1999-07-28  
 : PRIOR APPLICATION NUMBER: PCT/US99/20594  
 : PRIOR FILING DATE: 1999-09-13  
 : PRIOR APPLICATION NUMBER: PCT/US99/20944  
 : PRIOR FILING DATE: 1999-09-15  
 : PRIOR APPLICATION NUMBER: PCT/US99/21090  
 : PRIOR FILING DATE: 1999-11-29  
 : PRIOR APPLICATION NUMBER: PCT/US99/28214  
 : PRIOR FILING DATE: 1999-11-30  
 : PRIOR APPLICATION NUMBER: PCT/US99/28313  
 : PRIOR FILING DATE: 1999-12-02  
 : PRIOR APPLICATION NUMBER: PCT/US99/28564  
 : PRIOR FILING DATE: 1999-12-02  
 : PRIOR APPLICATION NUMBER: PCT/US99/30095  
 : PRIOR FILING DATE: 1999-12-16  
 : PRIOR APPLICATION NUMBER: PCT/US00/00219  
 : PRIOR FILING DATE: 2000-01-05  
 : NUMBER OF SEQ ID NOS: 423  
 : SEQ ID NO 16  
 : LENGTH: 30  
 : TYPE: DNA  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Synthetic Oligonucleotide Probe  
 : US-09-903-943-16



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: LENGTH: 50
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-904-956-16
:
Query Match      13.0% Score 15.6; DB 9; Length 50;
Best Local Similarity 81.8%; Pred. No. 2.7e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      86 CGATGGCTTCCATACCTGCTG 107
Db       29 CGATCGGATCCACACGCTGCTG 8

RESULT 83
US-09-907-794-16/c
: Sequence 16, Application US/09907794
: Publication No. US20030049677A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/907.794
: PRIOR FILING DATE: 2001-07-17
: PRIOR APPLICATION NUMBER: 09/665,350
: PRIOR FILING DATE: 2000-09-18
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214

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: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02/US99/28565
: PRIOR APPLICATION NUMBER: PCT/US99/28565
: PRIOR FILING DATE: 1999-12-02/US99/30095
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 2000-01 05
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 16
: LENGTH: 50
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-907-794-16
:
Query Match      13.0% Score 15.6; DB 9; Length 50;
Best Local Similarity 81.8%; Pred. No. 2.7e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      86 CGATGGCTTCCATACCTGCTG 107
Db       29 CGATCGGATCCACACGCTGCTG 8

RESULT 84
US-09-902-692-16/c
: Sequence 16, Application US/09902692
: Publication No. US20030034400A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/902.692
: PRIOR FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698

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APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/904.119  
PRIOR FILING DATE: 2001-07-11  
PRIOR FILING DATE: 2000-05-18  
PRIOR FILING DATE: 2000-02-22  
PRIOR FILING DATE: 1999-07-07  
PRIOR FILING DATE: 1999-07-26  
PRIOR FILING DATE: 1999-07-28  
PRIOR FILING DATE: 1999-09-08  
PRIOR FILING DATE: 1999-09-13  
PRIOR FILING DATE: 1999-09-15  
PRIOR FILING DATE: 1999-09-15  
PRIOR FILING DATE: 1999-09-15  
PRIOR FILING DATE: 1999-10-05  
PRIOR FILING DATE: 1999-11-29  
PRIOR FILING DATE: 1999-12-20  
PRIOR FILING DATE: 1999-12-20  
PRIOR FILING DATE: 1999-12-20  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 16  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE: OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-904-119:16  
Query Match 13.04; Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.84; Pred. No. 2.7e+04;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Caps 0;  
OY 86ICCATGGCTTCATAGCTGCTG 107  
DB 29 CGATCGGATGCCACGCTGCTG 8

RESULT 82  
US-09-904-956-16/c  
Sequence 16, Application US/09934956  
Publication No. US20030049622A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/904.956  
PRIOR FILING DATE: 2001-07-12  
PRIOR FILING DATE: 2000-02-22  
PRIOR FILING DATE: 1999-07-07  
PRIOR FILING DATE: 1999-07-26  
PRIOR FILING DATE: 1999-07-28  
PRIOR FILING DATE: 1999-09-08  
PRIOR FILING DATE: 1999-09-13  
PRIOR FILING DATE: 1999-09-15  
PRIOR FILING DATE: 1999-09-15  
PRIOR FILING DATE: 1999-10-05  
PRIOR FILING DATE: 1999-11-29  
PRIOR FILING DATE: 1999-12-20  
PRIOR FILING DATE: 1999-12-20  
PRIOR FILING DATE: 1999-12-20  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 16

PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 16  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-903-786-16

Query Match 13.0% Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8% Pred. No. 2.7e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 86 CGATGGCTTCACAGCTGCTG 107  
DB 29 CGATGGATCCACAGCTGCTG 8

RESULT 80  
US-09-902-736-16/c  
Sequence 16, Application US/09902736  
Publication No. US20030049676A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Paton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pen, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Summers, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-114  
CURRENT APPLICATION NUMBER: US/09/902,736  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 16  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-902-736-16  
Query Match 13.0% Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8% Pred. No. 2.7e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 86 CGATGGCTTCACAGCTGCTG 107  
DB 29 CGATGGATCCACAGCTGCTG 8  
RESULT 81  
US-09-904-119-16/c  
Sequence 16, Application US/09904119  
Publication No. US20030049621A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Paton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: God, Wei-Qiang

```
; OTHER INFORMATION: oligonucleotide probe
US-09-902-903-16
Query Match      13.0%  Score 15.6; DB 9; Length 50;
Best Local Similarity 81.8%; Pred. No. 2.7e+04;
Matches 18: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 86 CGATTGGCTTCATAGCTGCTG 107
    ||||| || |||| |||||
Db 29 CGATCGATGCCACAGCTGCTG 8

RESULT 78
US-09-903-749A-16/c
; Sequence 16, Application US/09903749A
; Publication No. US20030045693A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerttsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02

Query Match      13.0%  Score 15.6; DB 9; Length 50;
Best Local Similarity 81.8%; Pred. No. 2.7e+04;
Matches 18: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 86 CGATTGGCTTCATAGCTGCTG 107
    ||||| || |||| |||||
Db 29 CGATCGATGCCACAGCTGCTG 8

RESULT 79
US-09-903-786-16/c
; Sequence 16, Application US/09903786
; Publication No. US20030044793A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerttsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
```

APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William J.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US 09/906,700

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-11

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/30959

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US00/00219

PRIOR FILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 16

LENGTH: 50

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Oligonucleotide probe

US-09-906-700-16

Query Match 13.0% Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8%; Pred.No.27ex04;  
Matches 18; Conservative 4; Mismatches 4; Indels C; Gaps J.

DY 86 CGATTGGCTCCACTACGCTG 107  
||||| |||| | |||| | |||| | ||||  
DB 29 CGATCGATGCCAGCACTGCTG 8

RESULT 77  
US-09-902-903-16/C  
Sequence 16, Application US/09902903

Publication No. US20030044839A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Besnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Melvonne

APPLICANT: Flier, Steven H.

APPLICANT: Hong, Wei-Qiang

APPLICANT: Koopman, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Grifflsen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Maier, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Timms, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William J.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/902,903

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/30959

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US00/00219

PRIOR FILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 16

LENGTH: 50

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Oligonucleotide probe

US-09-906-700-16

Query Match 13.0% Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8%; Pred.No.27ex04;  
Matches 18; Conservative 4; Mismatches 4; Indels C; Gaps J.

DY 86 CGATTGGCTCCACTACGCTG 107  
||||| |||| | |||| | |||| | ||||  
DB 29 CGATCGATGCCAGCACTGCTG 8

RESULT 77  
US-09-902-903-16/C  
Sequence 16, Application US/09902903

Publication No. US20030044839A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Besnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Melvonne

APPLICANT: Flier, Steven H.

APPLICANT: Hong, Wei-Qiang

APPLICANT: Koopman, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Grifflsen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Maier, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Timms, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William J.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/902,903

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/30959

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US00/00219

PRIOR FILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 16

LENGTH: 50

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Oligonucleotide probe

US-09-906-700-16

Query Match 13.0% Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8%; Pred.No.27ex04;  
Matches 18; Conservative 4; Mismatches 4; Indels C; Gaps J.

DY 86 CGATTGGCTCCACTACGCTG 107  
||||| |||| | |||| | |||| | ||||  
DB 29 CGATCGATGCCAGCACTGCTG 8

RESULT 77  
US-09-902-903-16/C  
Sequence 16, Application US/0990290

APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavini, Ivor J.  
APPLICANT: Mathar, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/904.786  
CURRENT FILING DATE: 2001-07-12  
PRIOR APPLICATION NUMBER: 09/665,350  
PRIOR FILING DATE: 2000-09-18  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO: 16  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide Probe  
US-09-904-786-16  
Query Match 13.0% Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8%; Pred. No. 2.7e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 86 CGATTGGCTTCATAGCTGCTG 107  
DB 29 CGATCGGATGCCACAGCTGCTG 8  
RESULT 75  
US-09-906-646-16/c  
Sequence 16, Application US/09906646  
Publication No. US2003003997A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavini, Ivor J.  
APPLICANT: Mathar, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/906.646  
CURRENT FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO: 16  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: oligonucleotide probe  
US-09-906-646-16  
Query Match 13.0% Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8%; Pred. No. 2.7e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 86 CGATTGGCTTCATAGCTGCTG 107  
DB 29 CGATCGGATGCCACAGCTGCTG 8  
RESULT 76  
US-09-906-730-16/c  
Sequence 16, Application US/09906700  
Publication No. US2003003997A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.



PRIOR FILING DATE: 1999-09-08  
PCT APPLICATION NUMBER: PCT/US99/20944  
PCT FILING DATE: 1999-09-13  
PCT APPLICATION NUMBER: PCT/US99/21090  
PCT FILING DATE: 1999-09-15  
PCT APPLICATION NUMBER: PCT/US99/21547  
PCT FILING DATE: 1999-09-15  
PCT APPLICATION NUMBER: PCT/US99/23089  
PCT FILING DATE: 1999-10-05  
PCT APPLICATION NUMBER: PCT/US99/28214  
PCT FILING DATE: 1999-11-29  
PCT APPLICATION NUMBER: PCT/US99/28313  
PCT FILING DATE: 1999-12-02  
PCT APPLICATION NUMBER: PCT/US99/28564  
PCT FILING DATE: 1999-12-02  
PCT APPLICATION NUMBER: PCT/US99/28565  
PCT FILING DATE: 1999-12-02  
PCT APPLICATION NUMBER: PCT/US99/30095  
PCT FILING DATE: 1999-12-16  
PCT APPLICATION NUMBER: PCT/US99/30911  
PCT FILING DATE: 1999-12-20  
PCT APPLICATION NUMBER: PCT/US99/30999  
PCT FILING DATE: 1999-12-20  
PCT APPLICATION NUMBER: PCT/US00/00219  
PCT FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 6  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-304-859-16

Query Match 13.0% Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8%; Pred. No. 2.7e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 86 CGATGGCTTCGATGCTGCTG 107  
DB 29 CGATCGATGCCACGCTGCTG 8

RESULT 73  
US-09-309-204-16/c  
Sequence 16; Application US/0909204  
Publication No. US20030036061A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Dostaler, David  
APPLICANT: Dostaler, Luc  
APPLICANT: Eaton, Dan L  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurley, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Johnson, Gary J.  
APPLICANT: Kober, Jamie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: 10466-11  
CURRENT APPLICATION NUMBER: US/09/309,204  
CURRENT FILING DATE: 2001-07-18  
PCT APPLICATION NUMBER: PCT/US00/04414  
PCT FILING DATE: 2000-02-22  
PCT APPLICATION NUMBER: US 60/143,048  
PCT FILING DATE: 1999-07-07  
PCT APPLICATION NUMBER: US 60/145,698  
PCT FILING DATE: 1999-07-26  
PCT APPLICATION NUMBER: US 60/146,222  
PCT FILING DATE: 1999-07-28  
PCT APPLICATION NUMBER: PCT/US99/20594  
PCT FILING DATE: 1999-09-08  
PCT APPLICATION NUMBER: PCT/US99/20944  
PCT FILING DATE: 1999-09-13  
PCT APPLICATION NUMBER: PCT/US99/21090  
PCT FILING DATE: 1999-09-15  
PCT APPLICATION NUMBER: PCT/US99/21547  
PCT FILING DATE: 1999-09-15  
PCT APPLICATION NUMBER: PCT/US99/23089  
PCT FILING DATE: 1999-10-05  
PCT APPLICATION NUMBER: PCT/US99/28214  
PCT FILING DATE: 1999-11-29  
PCT APPLICATION NUMBER: PCT/US99/28313  
PCT FILING DATE: 1999-12-02  
PCT APPLICATION NUMBER: PCT/US99/28564  
PCT FILING DATE: 1999-12-02  
PCT APPLICATION NUMBER: PCT/US99/28565  
PCT FILING DATE: 1999-12-02  
PCT APPLICATION NUMBER: PCT/US99/30095  
PCT FILING DATE: 1999-12-16  
PCT APPLICATION NUMBER: PCT/US99/30911  
PCT FILING DATE: 1999-12-20  
PCT APPLICATION NUMBER: PCT/US99/30999  
PCT FILING DATE: 1999-12-20  
PCT APPLICATION NUMBER: PCT/US00/00219  
PCT FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 16  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-309-204-16

Query Match 13.0% Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8%; Pred. No. 2.7e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 86 CGATGGCTTCGATGCTGCTG 107  
DB 29 CGATCGATGCCACGCTGCTG 8

RESULT 74  
US-09-304-786-15/c  
Sequence 16; Application US/09904786  
Publication No. US20030035969A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Dostaler, David  
APPLICANT: Dostaler, Luc  
APPLICANT: Eaton, Dan L  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter

US-09-907-942-16

Query Match 13.0% Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8% Pred. No. 2.7e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 86 CGATTGGCTTCCATAGCTGCTG 107

Db 29 CGATCGATGCCACAGCTGCTG 8

RESULT 71

US-09-904-820-16/c

Sequence 16, Application US/09904820

Publication No. US20030036094A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewatt, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/904.820

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: 09/565.350

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143.048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145.698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146.222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/30999

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US00/00219

PRIOR FILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 16

LENGTH: 50

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Oligonucleotide Probe

US-09-904-820-16

Query Match 13.0% Score 15.6; DB 9; Length 50;

Best Local Similarity 81.8% Pred. No. 2.7e+04;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 86 CGATTGGCTTCCATAGCTGCTG 107

Db 29 CGATCGATGCCACAGCTGCTG 8

RESULT 72

US-09-904-859-16/c

Sequence 16, Application US/09904859

Publication No. US20030036060A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewatt, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/904.859

PRIOR FILING DATE: 2001-07-12

PRIOR APPLICATION NUMBER: 09/665.350

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143.048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145.698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146.222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

```

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavins, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-17
PRIORITY APPLICATION NUMBER: US/09/907,613
PRIORITY FILING DATE: 2000-02-22
PRIORITY APPLICATION NUMBER: US 60/143,048
PRIORITY FILING DATE: 1999-07-07
PRIORITY APPLICATION NUMBER: US 60/145,698
PRIORITY FILING DATE: 1999-07-26
PRIORITY APPLICATION NUMBER: US 60/146,222
PRIORITY FILING DATE: 1999-07-28
PRIORITY APPLICATION NUMBER: PCT/US99/20594
PRIORITY FILING DATE: 1999-09-08
PRIORITY APPLICATION NUMBER: PCT/US99/20944
PRIORITY FILING DATE: 1999-09-13
PRIORITY APPLICATION NUMBER: PCT/US99/21090
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/21547
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/23089
PRIORITY FILING DATE: 1999-10-05
PRIORITY APPLICATION NUMBER: PCT/US99/28214
PRIORITY FILING DATE: 1999-11-30
PRIORITY APPLICATION NUMBER: PCT/US99/28313
PRIORITY FILING DATE: 1999-11-30
PRIORITY APPLICATION NUMBER: PCT/US99/28564
PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/28565
PRIORITY FILING DATE: 1999-12-16
PRIORITY APPLICATION NUMBER: PCT/US99/30095
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US99/30911
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US99/30999
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 16
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
us-09-907-613-16

Query Match 13-08: Score 15.6; DB 9; Length 50;
Best Local Similarity 81.84; Pred. No. 2.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 86 CGATGCTTCACATAGCTGTC 107
DB 29 CGATCGATCCACAGCTGTC 8

RESULT 70
US-09-907-942-16/c
: Sequence 16, Application US/09907942
: Publication No. US20030027146A1

```

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Flvair, Brian

APPLICANT: Fong, Sheng

APPLICANT: Goss, Wei-Chang

APPLICANT: Geber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavins, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: 10466-14

CURRENT FILING DATE: 2002-01-22

PRIORITY APPLICATION NUMBER: PCT/US00/04414

PRIORITY FILING DATE: 2000-07-22

PRIORITY APPLICATION NUMBER: US 60/143,048

PRIORITY FILING DATE: 1999-07-07

PRIORITY APPLICATION NUMBER: US 60/145,698

PRIORITY FILING DATE: 1999-07-26

PRIORITY APPLICATION NUMBER: US 60/146,222

PRIORITY FILING DATE: 1999-07-28

PRIORITY APPLICATION NUMBER: PCT/US99/20594

PRIORITY FILING DATE: 1999-09-08

PRIORITY APPLICATION NUMBER: PCT/US99/20944

PRIORITY FILING DATE: 1999-09-13

PRIORITY APPLICATION NUMBER: PCT/US99/21090

PRIORITY FILING DATE: 1999-09-15

PRIORITY APPLICATION NUMBER: PCT/US99/21547

PRIORITY FILING DATE: 1999-09-15

PRIORITY APPLICATION NUMBER: PCT/US99/23089

PRIORITY FILING DATE: 1999-10-05

PRIORITY APPLICATION NUMBER: PCT/US99/28214

PRIORITY FILING DATE: 1999-11-29

PRIORITY APPLICATION NUMBER: PCT/US99/28313

PRIORITY FILING DATE: 1999-11-30

PRIORITY APPLICATION NUMBER: PCT/US99/28564

PRIORITY FILING DATE: 1999-12-02

PRIORITY APPLICATION NUMBER: PCT/US99/28565

PRIORITY FILING DATE: 1999-12-02

PRIORITY APPLICATION NUMBER: PCT/US99/30095

PRIORITY FILING DATE: 1999-12-16

PRIORITY APPLICATION NUMBER: PCT/US99/30911

PRIORITY FILING DATE: 1999-12-20

PRIORITY APPLICATION NUMBER: PCT/US99/30999

PRIORITY FILING DATE: 1999-12-20

PRIORITY APPLICATION NUMBER: PCT/US00/00219

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 16

LENGTH: 50

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Oligonucleotide probe

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1  : PRIOR APPLICATION NUMBER: PCT/US99/21547
2  : PRIOR FILING DATE: 1999-09-15
3  : PRIOR APPLICATION NUMBER: PCT/US99/23089
4  : PRIOR FILING DATE: 1999-10-05
5  : PRIOR APPLICATION NUMBER: PCT/US99/28214
6  : PRIOR FILING DATE: 1999-11-29
7  : PRIOR APPLICATION NUMBER: PCT/US99/28313
8  : PRIOR FILING DATE: 1999-11-30
9  : PRIOR APPLICATION NUMBER: PCT/US99/28564
10 : PRIOR FILING DATE: 1999-12-02
11 : PRIOR APPLICATION NUMBER: PCT/US99/28565
12 : PRIOR FILING DATE: 1999-12-02
13 : PRIOR APPLICATION NUMBER: PCT/US99/30095
14 : PRIOR FILING DATE: 1999-12-16
15 : PRIOR APPLICATION NUMBER: PCT/US99/30911
16 : PRIOR FILING DATE: 1999-12-20
17 : PRIOR APPLICATION NUMBER: PCT/US99/30999
18 : PRIOR FILING DATE: 1999-12-20
19 : PRIOR APPLICATION NUMBER: PCT/US00/000219
20 : PRIOR FILING DATE: 2000-01-05
21 : NUMBER OF SEQ IDS NOS: 423
22 : SEQ ID NO: 16
23 : LENGTH: 50
24 : TYPE: DNA
25 : ORGANISM: Artificial Sequence
26 : FEATURE:
27 : OTHER INFORMATION: Synthetic Oligonucleotide
28 : US-9306-745-16

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1  PRIOR APPLICATION NUMBER: 09/665,350
2  PRIOR FILING DATE: 2000-09-18
3  PRIOR APPLICATION NUMBER: PCT/US00/04414
4  PRIOR FILING DATE: 2000-02-22
5  PRIOR APPLICATION NUMBER: US 60/143,048
6  PRIOR FILING DATE: 1999-07-07
7  PRIOR APPLICATION NUMBER: US 60/145,698
8  PRIOR FILING DATE: 1999-07-26
9  PRIOR APPLICATION NUMBER: US 60/146,222
10 PRIOR FILING DATE: 1999-07-28
11 PRIOR APPLICATION NUMBER: PCT/US99/20594
12 PRIOR FILING DATE: 1999-09-08
13 PRIOR APPLICATION NUMBER: PCT/US99/20944
14 PRIOR FILING DATE: 1999-09-13
15 PRIOR APPLICATION NUMBER: PCT/US99/21090
16 PRIOR FILING DATE: 1999-09-15
17 PRIOR APPLICATION NUMBER: PCT/US99/21547
18 PRIOR FILING DATE: 1999-09-15
19 PRIOR APPLICATION NUMBER: PCT/US99/23089
20 PRIOR FILING DATE: 1999-10-05
21 PRIOR APPLICATION NUMBER: PCT/US99/28214
22 PRIOR FILING DATE: 1999-11-29
23 PRIOR APPLICATION NUMBER: PCT/US99/28313
24 PRIOR FILING DATE: 1999-11-30
25 PRIOR APPLICATION NUMBER: PCT/US99/28564
26 PRIOR FILING DATE: 1999-12-02
27 PRIOR APPLICATION NUMBER: PCT/US99/28565
28 PRIOR FILING DATE: 1999-12-02
29 PRIOR APPLICATION NUMBER: PCT/US99/30095
30 PRIOR FILING DATE: 1999-12-16
31 PRIOR APPLICATION NUMBER: PCT/US99/30911
32 PRIOR FILING DATE: 1999-12-20
33 PRIOR APPLICATION NUMBER: PCT/US99/30999
34 PRIOR FILING DATE: 1999-12-20
35 PRIOR APPLICATION NUMBER: PCT/US00/00219
36 PRIOR FILING DATE: 2000-01-05
37 NUMBER OF SEQ ID NOS: 423
38
39 SEQ ID NO 16
40 LENGTH: 50
41 TYPE: DNA
42 ORGANISM: Artificial Sequence
43 FEATURE:
44 OTHER INFORMATION: Synthetic Oligonucleotide
45 US-09-906-838-16

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OY      86  CGATTGGCTTCATAGCTGCTG 107
      |||| || |||| |||||
DB      29  CGATCGGATGCCACAGCTGCTG 8

RESULT 66
US-09-904-011-16/c
: Sequence 16, Application US/09904011
: Publication No. US2003003530A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gueney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pao, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/904,011
: PRIOR FILING DATE: 2001-07-11
: PRIOR APPLICATION NUMBER: 09/665,350
: PRIOR FILING DATE: 2000-09-18
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/28565
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20

: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/03219
: PRIOR FILING DATE: 2000-01-05
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 16
: LENGTH: 50
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-904-011-16

Query Match      13.0%  Score 15.6;  DB 9;  Length 50;
Best Local Similarity 81.8%;  Pred. No. 2.7e+04;
Matches 18;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0:

OY      86  CGATTGGCTTCATAGCTGCTG 107
      |||| || |||| |||||
DB      29  CGATCGGATGCCACAGCTGCTG 8

RESULT 67
US-09-906-742-16/c
: Sequence 16, Application US/09906742
: Publication No. US20030023054A
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gueney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pao, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/906,742
: PRIOR FILING DATE: 2001-07-16
: PRIOR APPLICATION NUMBER: 09/665,350
: PRIOR FILING DATE: 2000-09-18
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
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: PRIOR APPLICATION NUMBER: PCT/US99/21089
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: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/28565
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
```

APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavir, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/907,824  
CURRENT FILING DATE: 2001-07-17  
PRIOR APPLICATION NUMBER: 09/665,350  
PRIOR FILING DATE: 2000-09-16  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 16  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-907-824-16

Query Match 13.0% Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8%; Pred. No. 2.7e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 86 CGATTGGCTTCATAGCTGCTG 107

Db 29 CGATGGATGCCACAGCTGCTG 8  
RESULT 65  
US-09-907-841-16/c  
Sequence 16, Application US/09907841  
Publication No. US20020198366A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavir, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/907,841  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 16  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: oligonucleotide probe  
US-09-907-841-16

Query Match 13.0% Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8%; Pred. No. 2.7e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 16  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-905-291A-16

Query Match 13.0% Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8%; Pred. No. 2.7e-04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 86 CGATTGGCTTCATGCTGCTG 107  
||||| || |||| |||||  
Db 29 CGATCGATGCCACGCTGCTG 8

## RESULT 63

US-09-902-853-16/c  
Sequence 16, Application US/09902853  
Publication No. US20020192659A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Guiney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavits, Ivar J.  
APPLICANT: Mathier, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/902,853  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: US/09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 16  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide probe  
US-09-902-853-16

Query Match 13.0% Score 15.6; DB 9; Length 50;  
Best Local Similarity 81.8%; Pred. No. 2.7e-04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 86 CGATTGGCTTCATGCTGCTG 107  
||||| || |||| |||||  
Db 29 CGATCGATGCCACGCTGCTG 8

## RESULT 64

US-09-907-824-16/c  
Sequence 16, Application US/09907824  
Publication No. US20020197671A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen

```

: APPLICANT: HUDSON, Peter John
: APPLICANT: KORTT, Alex Andrew
: APPLICANT: IRVING, Robert Alexander
: APPLICANT: ATWELL, John Leslie
: TITLE OF INVENTION: HIGH AVIDITY POLYVALENT AND POLYSPECIFIC REAGENTS
: FILE REFERENCE: 016786/0212
: CURRENT APPLICATION NUMBER: US/09/147,142
: EARLIER FILING DATE: 1999-03-05
: EARLIER APPLICATION NUMBER: PCT/AU98/00212
: EARLIER FILING DATE: 1998-03-26
: EARLIER APPLICATION NUMBER: AU PO 5917
: EARLIER FILING DATE: 1997-03-27
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 11
: LENGTH: 45
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: synthetic
: OTHER INFORMATION: oligonucleotide used to insert codon between VH
: OTHER INFORMATION: and VL domains of NC10 scFv-0
: US-09-147-142-11
:
: Query Match 13.0% Score 15.6; DB 10; Length 45;
: Best Local Similarity 53.2% Pred. No. 2.6e+04;
: Matches 24; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
:
: QY 30 ACCTCATATCCCACTCCAGGAGGATTCAGGGGTCC 67
: | | | | | | | | | | | | | | | | | | | |
: Db 38 AGCTCGATATCACCACCGGAGCGGTGACCGTGCTCC 1
:
: RESULT 60
: US-09-147-142-12
: Sequence 12, Application US/09147142
: Patent No. US20020018749A1
: GENERAL INFORMATION:
: APPLICANT: HUDSON, Peter John
: APPLICANT: KORTT, Alex Andrew
: APPLICANT: IRVING, Robert Alexander
: APPLICANT: ATWELL, John Leslie
: TITLE OF INVENTION: HIGH AVIDITY POLYVALENT AND POLYSPECIFIC REAGENTS
: FILE REFERENCE: 016786/0212
: CURRENT APPLICATION NUMBER: US/09/147,142
: EARLIER FILING DATE: 1999-03-05
: EARLIER APPLICATION NUMBER: PCT/AU98/00212
: EARLIER FILING DATE: 1998-03-26
: EARLIER APPLICATION NUMBER: AU PO 5917
: EARLIER FILING DATE: 1997-03-27
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 12
: LENGTH: 45
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: synthetic
: OTHER INFORMATION: oligonucleotide used to insert codon between VH
: OTHER INFORMATION: and VL domains of NC10 scFv-0
: US-09-147-142-12
:
: Query Match 13.0% Score 15.6; DB 10; Length 45;
: Best Local Similarity 53.2% Pred. No. 2.6e+04;
: Matches 24; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
:
: QY 30 ACCTCATATCCCACTCCAGGAGGATTCAGGGGTCC 67
: | | | | | | | | | | | | | | | | | | | |
: Db 8 AGCTCGATATCACCACCGGAGCGGTGACCGTGCTCC 45
:
: RESULT 61
: US-09-896-915-9
:
: Sequence 9, Application US/09896915
: Patent No. US20020119459A1
: GENERAL INFORMATION:
: APPLICANT: Medical Research Council
: APPLICANT: Griffiths, Andrew
: TITLE OF INVENTION: Optical Sorting Method
: FILE REFERENCE: 18396/2022
: CURRENT APPLICATION NUMBER: US/09/896,915
: CURRENT FILING DATE: 2001-06-29
: PRIOR APPLICATION NUMBER: GB9900298.2
: PRIOR FILING DATE: 1999-01-07
: PRIOR APPLICATION NUMBER: PCT/GB00/00030
: PRIOR FILING DATE: 2000-01-06
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 9
: LENGTH: 49
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Oligonucleotide EDHFR-FO
: US-09-896-915-9
:
: Query Match 13.0% Score 15.6; DB 10; Length 49;
: Best Local Similarity 81.8% Pred. No. 2.2e+04;
: Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
:
: QY 30 ACCTCATATCCCACTCCAGGAGGATTCAGGGGTCC 51
: | | | | | | | | | | | | | | | | | | | |
: Db 13 ACCTTATTACCGCGCTCCAGGAGGATTCAGGGGTCC 34
:
: RESULT 62
: US-09-905-291A-16/c
: Sequence 16, Application US/09905291A
: Patent No. US20020160374A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Flvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kijavini, Ivar J.
: APPLICANT: Mather, Jeannie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/905,291A
: CURRENT FILING DATE: 2001-07-12
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26

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PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 323  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-907-652-323

Query Match 13.24; Score 15.8; DB 9; Length 45;  
Best Local Similarity 74.1%; Pred. No. 2.2e+04;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Oy 29 CACCTCATTATCCCACTCCAGAGGGA 55  
Db 28 CCCACATATCCACAGCCAGAGGGA 2

RESULT 55  
US-09-909-320-323/c  
Sequence 323. Application US/090909120  
Patent No. US20020132240A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Goddard, A.  
APPLICANT: Goddard, A.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Math, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/909,320

CURRENT FILING DATE: 2002-01-04  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 323  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-909-320-323

Query Match 13.24; Score 15.8; DB 10; Length 45;  
Best Local Similarity 74.1%; Pred. No. 2.2e+04;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Oy 29 CACCTCATTATCCCACTCCAGAGGGA 55  
Db 28 CCCACATATCCACAGCCAGAGGGA 2

RESULT 56  
US-09-909-088B-323/c  
Sequence 323. Application US/0909088B  
Patent No. US20020146709A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Goddard, A.  
APPLICANT: Goddard, A.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.



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: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/903,925
: PRIOR FILING DATE: 2001-07-11
: PRIOR APPLICATION NUMBER: 09/665,350
: PRIOR FILING DATE: 2000-09-18
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/28565
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/00219
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 323
: LENGTH: 45
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic Oligonucleotide Probe
: US-09-903-925-323

Query Match 13.2%; Score 15.8; DB 9; Length 45;
Best Local Similarity 74.1%; Pred. No. 2.2e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 29 CACCTCATTCATCCCACTCCAGAGGGA 55
   ||| ||| ||| ||| ||| ||| |||
DB 28 CCCACATACCTCCAGCCAGAGGGA 2

RESULT 52
US-09-906-760A-323/c
: Sequence 323. Application US/09906760A

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: Publication No. US20030096340A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gjeritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/906,760A
: CURRENT FILING DATE: 2001-07-16
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/28565
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/00219
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 323
: LENGTH: 45
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic Oligonucleotide Probe

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RESULT 50
US-09-902-615-323/C
: Sequence 323, Application US/09902615
: Publication No. US/0030092002A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, L.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: Acids Encoding the Same
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/902,615
: CURRENT FILING DATE: 2001-12-14
: Prior application data removed. Check file wrapper or PALM.
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 323
: LENGTH: 45
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-902-615-323
Query Match 13.2% Score 15.8; DB 9; Length 45;
Best Local Similarity 74.1% Pred. No. 2.2e-04;
Matches 20; Conservative 3; Mismatches 7; Indels 0; Caps 0.
QY 29 CACCTCATTCCTCCACAGGCA 55
DDB 1 CACCTCATTCCTCCACAGGCA 55
28 CCCCATACTCCACAGCCACAGGCA 2
RESULT 51
US-09-903-925-323/C
: Sequence 323, Application US/09901925
: Publication No. US/2003009623A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.

```

PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 323  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-902-634-323

Query Match 13.2% Score 15.8; DB 9; Length 45;  
Best Local Similarity 74.1% Pred. No. 2.2e+04;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 29 CACCTCATTATCCCCACTCCAGAGGA 55  
DB 28 CCCACATACCTCCACAGCCCGAGAGGA 2

## RESULT 48

US-09-902-713-323/c  
Sequence 323, Application US/09902713  
Publication No. US20030082541A1

## GENERAL INFORMATION:

APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavoin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: US/09/902,713

PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 09/665,350

PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999

PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219

PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 323  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-902-713-323

Query Match 13.2% Score 15.8; DB 9; Length 45;  
Best Local Similarity 74.1% Pred. No. 2.2e+04;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 29 CACCTCATTATCCCCACTCCAGAGGA 55

DB 28 CCCACATACCTCCACAGCCCGAGAGGA 2

## RESULT 49

US-09-907-979-323/c

Sequence 323, Application US/09907979

Publication No. US20030082542A1

## GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang



1 PCT APPLICATION NUMBER: PCT/US00/002191  
 2  
 3 PRIORITY FILING DATE: 2000-01-05  
 4  
 5 NUMBER OF SEQ ID NOS: 423  
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Query Match 13.2%; Score 15.8; DB 9; Length 45;  
Best Local Similarity 74.1%; Pred. No. 2.2e+04;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

RESULT 44 :  
US-09-907-575-323/c  
: Sequence 323, Application US/09907575  
: Publication No. US20030073079A1

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1  / PRIOR APPLICATION NUMBER: PCT/US99/282124
2  / PRIOR FILING DATE: 1999-11-29
3  / PRIOR APPLICATION NUMBER: PCT/US99/28313
4  / PRIOR FILING DATE: 1999-11-30
5  / PRIOR APPLICATION NUMBER: PCT/US99/28564
6  / PRIOR FILING DATE: 1999-12-02
7  / PRIOR APPLICATION NUMBER: PCT/US99/28565
8  / PRIOR FILING DATE: 1999-12-02
9  / PRIOR APPLICATION NUMBER: PCT/US99/30095
10 / PRIOR FILING DATE: 1999-12-16
11 / PRIOR APPLICATION NUMBER: PCT/US99/30911
12 / PRIOR FILING DATE: 1999-12-20
13 / PRIOR APPLICATION NUMBER: PCT/US99/30999
14 / PRIOR FILING DATE: 1999-12-20
15 / PRIOR APPLICATION NUMBER: PCT/US00/00219
16 / PRIOR FILING DATE: 2000-01-05
17 / NUMBER OF SEQ ID NOS: 423
18 / SEQ ID NO 323
19 / LENGTH: 45
20 / TYPE: DNA
21 / ORGANISM: Artificial Sequence
22 / OTHER INFORMATION: Synthetic Oligonucleotide
23 / FEATURE:
24 / US-907-575-323

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Query Match      13.28; Score 15.8; DB 9; Length 45;
Best Local Similarity 74.18; Pred. No. 2 2e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

RESULT 45

US-09-902-759-323/c

Sequence 323, Application US/09902759

PUBLICATION NO. US20030077654A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Flivaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Harry E.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Kijavin, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/902,759

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07



```

: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tunnas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/909,064
: CURRENT FILING DATE: 2001-07-18
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/28565
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/00219
: PRIOR FILING DATE: 2000-01-05
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 323
: LENGTH: 45
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic Oligonucleotide Probe
:
: Query Match 13.74; Score 15.8; DB 9; Length 45;
: Best Local Similarity 74.15; Pred. No. 2.2e-04;
: Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
:
: QY 29 CACCTCATCTCCCACTCCAGGCGA 55

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Db 28 CCCCATCTCCACAGCCGAGGGA 2
:
: RESULT 43
: US-09-905-088-323/C
: Sequence 323, Application US/09905088
: Publication No. US20030073077A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Bolstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tunnas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/905,088
: CURRENT FILING DATE: 2001-07-12
: PRIOR APPLICATION NUMBER: 09/665,350
: PRIOR FILING DATE: 2000-09-18
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/28565
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20

```



[illegible]



APPLICANT: Wood, William, I  
TITLE OF INVENTION: Sulfated and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Sulfated and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-74  
FILE REFERENCE: 10466-74  
CURRENT APPLICATION NUMBER: US/09/903,943  
CURRENT FILING DATE: 2001-07-11  
PRIOR APPLICATION NUMBER: 09/465,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02

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; PRIOR APPLICATION NUMBER: PCT/US99/30095
;
; PRIOR FILING DATE: 1999-12-16
;
; PRIOR APPLICATION NUMBER: PCT/US99/30911
;
; PRIOR FILING DATE: 1999-12-20
;

```

: PRIOR APPLICATION NUMBER: PCT/US99/30999  
 : PRIOR FILING DATE: 1999-12-20  
 : PRIOR APPLICATION NUMBER: PCT/US00/00219  
 : PRIOR FILING DATE: 2000-01-05

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1  SEQ ID NO 323
2  LENGTH: 45
3  TYPE: DNA
4  ORIGIN: Artificial Sequence
5  FEATURE INFORMATION: Synthetic Oligonucleotide Probe
6  US-09-903-943-323
7
8  Query Match      13.2%   Score 15.8   DB 9:   Length 45:
9  Best Local Similarity 74.1%   P: 0.2.2e+04:
10 Matches 20:  Conservative 0:  Mismatches 7:  Indels 0:  Gaps 0:
11
12  ID          29  CACCTATTATCCCACTCCAGAGGA 55
13              1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
14  ID          28  CCCCACATACTCCACAGCCCAAGAGCA 2
15
16  RESULT 37
17  : Sequence 323, Application US/9900462
18  : Publication No. US20030054351A1
19  : GENERAL INFORMATION:
20  : APPLICANT: Genentech, Inc
21  : APPLICANT: Alkermes, Inc
22  : APPLICANT: Boehringer-Ingelheim, Ltd
23  : APPLICANT: Desmovers, Inc
24  : APPLICANT: Eaton, Dan L
25  : APPLICANT: Ferrara, Napoleone
26  : APPLICANT: Filvaroff, Ellen
27  : APPLICANT: Fong, Sherman

```

ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic Oligonucleotide Probe  
 US-09-907-794-323

Query Match 13.2% Score 15.8; DB 9; Length 45;  
 Best Local Similarity 74.1% Pred. No. 2.2e+04;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 29 CACCTCATTTATCCCACTCCAGAGGGA 55  
 ||||| ||||| ||||| ||||| |||||  
 Db 28 CCCACATACCTCCAGAGGGA 2

## RESULT 34

US-09-902-692-323/c  
 Sequence 323, Application US/09902692  
 Publication No. US20030054400A1

## GENERAL INFORMATION:

APPLICANT: Genentech, Inc.  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, A.  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth, J.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Mather, Jennie P.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William, I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: 10466-14  
 CURRENT APPLICATION NUMBER: US/09/902,692  
 PRIOR FILING DATE: 2001-07-10  
 PRIOR APPLICATION NUMBER: PCT/US00/04414  
 PRIOR FILING DATE: 2000-02-22  
 PRIOR APPLICATION NUMBER: US 50/143,048  
 PRIOR FILING DATE: 1999-07-07  
 PRIOR APPLICATION NUMBER: US 50/145,698  
 PRIOR FILING DATE: 1999-07-26  
 PRIOR APPLICATION NUMBER: US 50/146,222  
 PRIOR FILING DATE: 1999-07-28  
 PRIOR APPLICATION NUMBER: PCT/US99/20594  
 PRIOR FILING DATE: 1999-09-08  
 PRIOR APPLICATION NUMBER: PCT/US99/20944  
 PRIOR FILING DATE: 1999-09-13  
 PRIOR APPLICATION NUMBER: PCT/US99/21090  
 PRIOR FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: PCT/US99/21547  
 PRIOR FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: PCT/US99/23089  
 PRIOR FILING DATE: 1999-10-05  
 PRIOR APPLICATION NUMBER: PCT/US99/28214  
 PRIOR FILING DATE: 1999-11-29  
 PRIOR APPLICATION NUMBER: PCT/US99/28313  
 PRIOR FILING DATE: 1999-11-30  
 PRIOR APPLICATION NUMBER: PCT/US99/28564  
 PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565  
 PRIOR FILING DATE: 1999-12-02  
 PRIOR APPLICATION NUMBER: PCT/US99/30095  
 PRIOR FILING DATE: 1999-12-16  
 PRIOR APPLICATION NUMBER: PCT/US99/30911  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: PCT/US99/30999  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: PCT/US00/00219  
 PRIOR FILING DATE: 2000-01-05  
 NUMBER OF SEQ ID NOS: 423  
 SEQ ID NO 323  
 TYPE: DNA  
 LENGTH: 45  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic Oligonucleotide Probe  
 US-09-902-692-323

Query Match 13.2% Score 15.8; DB 9; Length 45;  
 Best Local Similarity 74.1% Pred. No. 2.2e+04;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 29 CACCTCATTTATCCCACTCCAGAGGGA 55  
 ||||| ||||| ||||| ||||| |||||  
 Db 28 CCCACATACCTCCAGAGGGA 2

## RESULT 35

US-09-903-520-323/c  
 Sequence 323, Application US/09903520  
 Publication No. US20030054401A1

## GENERAL INFORMATION:

APPLICANT: Genentech, Inc.  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, A.  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth, J.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Mather, Jennie P.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William, I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: 10466-14  
 CURRENT APPLICATION NUMBER: US/09/903,520  
 PRIOR FILING DATE: 2001-07-11  
 PRIOR APPLICATION NUMBER: 09/665,350  
 PRIOR FILING DATE: 2000-09-18  
 PRIOR APPLICATION NUMBER: PCT/US00/04414  
 PRIOR FILING DATE: 2000-02-22  
 PRIOR APPLICATION NUMBER: US 60/143,048  
 PRIOR FILING DATE: 1999-07-07  
 PRIOR APPLICATION NUMBER: US 60/145,698  
 PRIOR FILING DATE: 1999-07-26  
 PRIOR APPLICATION NUMBER: PCT/US99/28564  
 PRIOR FILING DATE: 1999-07-28

APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/904.956  
PRIOR FILING DATE: 2001-07-12  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143.048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145.698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146.222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-11  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-11  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 323  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-904-956-323

Query Match 13.20; Score 15.8; DB 9; Length 45;  
Basic Local Similarity 74.1%; Pred. No. 2.2e+04;  
Matches 20; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 29 CACCTGATTATCCCACTCCAGAGGGA 55  
Db 28 CCCACATATCTCCAGAGGAGGGA 2

RESULT 33  
US-09-907-794-323/c

Sequence 323. Application US/09907794  
Publication No. US20030049677A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gac, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/907.794  
PRIOR FILING DATE: 2001-07-17  
PRIOR APPLICATION NUMBER: 09/665.350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143.048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145.698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146.222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 323  
LENGTH: 45  
TYPE: DNA

PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 323  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE: Synthetic Oligonucleotide Probe  
OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-902-736-323

Query Match 13.28; Score 15.8; DB 9; Length 45;  
Best Local Similarity 74.18; Pred. No. 2.2e+04;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 29 CACCTATTATCCACACGAGGGA 55  
DB 28 CCCACATCTCCACAGCCAGGGA 2

RESULT 31  
US-09-904-119-323/c  
Sequence 323; Application US/09-904119  
Publication No. US20030049621A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvarsoff, Ellen  
APPLICANT: Fong, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Goodwin, Paul J.  
APPLICANT: Grimsdell, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavitt, Ivar J.  
APPLICANT: Maher, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Williams, P. Hickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/904 119  
CURRENT FILING DATE: 2001-09-21  
PRIOR APPLICATION NUMBER: 2000-09-21  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-27  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,688  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,212  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20444  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28114  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28113  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28164  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28165  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30111  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30199  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00119  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 323  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE: Synthetic Oligonucleotide Probe  
OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-904-119-323

Query Match 13.28; Score 15.8; DB 9; Length 45;  
Best Local Similarity 74.18; Pred. No. 2.2e+04;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 29 CACCTATTATCCACACGAGGGA 55  
DB 28 CCCACATCTCCACAGCCAGGGA 2

RESULT 32  
US-09-904-956-323/c  
Sequence 323; Application US/09-904956  
Publication No. US20030049621A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvarsoff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.





APPLICANT:	Gurney, Austin L.
APPLICANT:	Hillan, Kenneth, J.
APPLICANT:	Kilavin, Ivar J.
APPLICANT:	Mather, Jennie P.
APPLICANT:	Pan, James
APPLICANT:	Paoli, Nicholas F.
APPLICANT:	Roy, Margaret Ann
APPLICANT:	Stewart, Timothy A.
APPLICANT:	Tunas, Daniel
APPLICANT:	Williams, P. Hickey
APPLICANT:	Wood, William, I.
TITLE OF INVENTION: Secured and Transmitted	
FILE REFERENCE: 10466-14	
CURRENT APPLICATION NUMBER:	US/09/902,903
CURRENT FILING DATE:	2001-07-10
PRIOR APPLICATION NUMBER:	PCT/US99/04414
PRIOR FILING DATE:	2000-02-22
PRIOR APPLICATION NUMBER:	US 60/143, 048
PRIOR FILING DATE:	1999-07-07
PRIOR APPLICATION NUMBER:	US 60/145, 698
PRIOR FILING DATE:	1999-07-26
PRIOR APPLICATION NUMBER:	US 60/146, 222
PRIOR FILING DATE:	1999-07-28
PRIOR APPLICATION NUMBER:	PCT/US99/20594
PRIOR FILING DATE:	1999-09-08
PRIOR APPLICATION NUMBER:	PCT/US99/20944
PRIOR FILING DATE:	1999-09-13
PRIOR APPLICATION NUMBER:	PCT/US99/21090
PRIOR FILING DATE:	1999-09-15
PRIOR APPLICATION NUMBER:	PCT/US99/21547
PRIOR FILING DATE:	1999-09-15
PRIOR APPLICATION NUMBER:	PCT/US99/23089
PRIOR FILING DATE:	1999-10-05
PRIOR APPLICATION NUMBER:	PCT/US99/28214
PRIOR FILING DATE:	1999-11-29
PRIOR APPLICATION NUMBER:	PCT/US99/28313
PRIOR FILING DATE:	1999-11-30
PRIOR APPLICATION NUMBER:	PCT/US99/28564
PRIOR FILING DATE:	1999-12-02
PRIOR APPLICATION NUMBER:	PCT/US99/28565
PRIOR FILING DATE:	1999-12-02
PRIOR APPLICATION NUMBER:	PCT/US99/30095
PRIOR FILING DATE:	1999-12-16
PRIOR APPLICATION NUMBER:	PCT/US99/30911
PRIOR FILING DATE:	1999-12-30
PRIOR APPLICATION NUMBER:	PCT/US99/30599
PRIOR FILING DATE:	1999-12-30
PRIOR APPLICATION NUMBER:	PCT/US00/00219
PRIOR FILING DATE:	2000-01-05
NUMBER OF SEQ ID NOS: 423	
SEQ ID NO 323	
LENGTH: 45	

APPLICANT: Genentech, Inc.  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Bolstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, A.  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillen, Kenneth, J.  
 APPLICANT: Klibavin, Ivar J.  
 APPLICANT: Malher, Jennie P.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William, I.  
 APPLICANT: Woods, William, I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides  
 FILE REFERENCE: 10466-14  
 CURRENT APPLICATION NUMBER: US/09/903 749A  
 CURRENT FILING DATE: 2001-07-11  
 PRIOR APPLICATION NUMBER: PCT/US00/04114  
 PRIOR FILING DATE: 2000-07-22  
 PRIOR APPLICATION NUMBER: US 60/143,048  
 PRIOR FILING DATE: 1999-07-07  
 PRIOR APPLICATION NUMBER: US 60/145,698  
 PRIOR FILING DATE: 1999-07-26  
 PRIOR APPLICATION NUMBER: US 60/146,222  
 PRIOR FILING DATE: 1999-07-28  
 PRIOR APPLICATION NUMBER: PCT/US99/20394  
 PRIOR FILING DATE: 1999-09-08  
 PRIOR APPLICATION NUMBER: PCT/US99/20344  
 PRIOR FILING DATE: 1999-09-13  
 PRIOR APPLICATION NUMBER: PCT/US99/21490  
 PRIOR FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: PCT/US99/21447  
 PRIOR FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: PCT/US99/23489  
 PRIOR FILING DATE: 1999-10-05  
 PRIOR APPLICATION NUMBER: PCT/US99/28214  
 PRIOR FILING DATE: 1999-11-29  
 PRIOR APPLICATION NUMBER: PCT/US99/28113  
 PRIOR FILING DATE: 1999-11-30  
 PRIOR APPLICATION NUMBER: PCT/US99/28564  
 PRIOR FILING DATE: 1999-12-03  
 PRIOR APPLICATION NUMBER: PCT/US99/28565  
 PRIOR FILING DATE: 1999-12-02  
 PRIOR APPLICATION NUMBER: PCT/US99/30395  
 PRIOR FILING DATE: 1999-12-16  
 PRIOR APPLICATION NUMBER: PCT/US99/30311  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: PCT/US99/30399  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: PCT/US00/00319  
 PRIOR FILING DATE: 2000-01-05  
 NUMBER OF SEQ ID NOS: 423  
 SEQ ID NO 323  
 LENGTH: 45  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetic Oligonucleotide Probe  
 09-903-749A-323

PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 323  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-906-700-323

Query Match 13.2% Score 15.8; DB 9; Length 45;  
Best Local Similarity 74.1% Pred. No. 2.2e+04;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 29 CACCTATTATCCCACTCCAGAGGA 55  
Db 28 CCCCATATCTCCAGCCAGAGGA 2

RESULT 26  
US-09-906-700-323/c  
Sequence 323, Application US/0906700  
Publication No. US200303972A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunes, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/906.700  
CURRENT FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 323  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide Probe  
US-09-906-700-323

Query Match 13.2% Score 15.8; DB 9; Length 45;  
Best Local Similarity 74.1% Pred. No. 2.2e+04;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 29 CACCTATTATCCCACTCCAGAGGA 55  
Db 28 CCCCATATCTCCAGCCAGAGGA 2

RESULT 27  
US-09-902-903-323/c  
Sequence 323, Application US/0902903  
Publication No. US20030044839A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.



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: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-904-820-323

Query Match      13.2%  Score 15.8; DB 9; Length 45;
Best Local Similarity 74.1%  Pred. No. 2.2e-04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 29 CACCTCATTATCCCACTCCAGAGGGA 55
    ||||| ||||| ||||| |||||
Db 28 CCCCATACTCCAGAGCCAGAGGGA 2

RESULT 22
US-09-904-859-323/c
: Sequence 323, Application US/09904859
: Publication No. US20030036050A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Denoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Hillen, Kenneth, J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/904,859
: PRIOR FILING DATE: 2001-07-12
: PRIOR FILING DATE: 2000-09-18
: PRIOR FILING DATE: 2000-02-22
: PRIOR FILING DATE: 2000-02-22
: PRIOR FILING DATE: 1999-07-07
: PRIOR FILING DATE: 1999-07-26
: PRIOR FILING DATE: 1999-07-28
: PRIOR FILING DATE: 1999-09-08
: PRIOR FILING DATE: 1999-09-13
: PRIOR FILING DATE: 1999-09-15
: PRIOR FILING DATE: 1999-09-15
: PRIOR FILING DATE: 1999-09-15
: PRIOR FILING DATE: 1999-10-05
: PRIOR FILING DATE: 1999-11-29
: PRIOR FILING DATE: 1999-11-30

: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-904-859-323

Query Match      13.2%  Score 15.8; DB 9; Length 45;
Best Local Similarity 74.1%  Pred. No. 2.2e-04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 29 CACCTCATTATCCCACTCCAGAGGGA 55
    ||||| ||||| ||||| |||||
Db 28 CCCCATACTCCAGAGCCAGAGGGA 2

RESULT 23
US-09-909-204-323/c
: Sequence 323, Application US/09909204
: Publication No. US20030036061A1
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Denoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gueney, Austin L.
: APPLICANT: Hillen, Kenneth, J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/909,204
: PRIOR FILING DATE: 2001-07-18
: PRIOR FILING DATE: 2000-02-22
: PRIOR FILING DATE: 2000-02-22
: PRIOR FILING DATE: 1999-07-07
: PRIOR FILING DATE: 1999-07-26
: PRIOR FILING DATE: 1999-07-26
: PRIOR FILING DATE: 1999-11-29
: PRIOR FILING DATE: 1999-11-30
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/907,613  
PRIORITY FILING DATE: 2001-07-17  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30959  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 323  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide Probe

Query Match      13.2%    Score 15.8; DB 9; Length 45;  
Best Local Similarity     74.1%; Pred. No. 2.2e+04;  
Matches        20; Conservative    0; Mismatches        7; Indels            0; Gaps            0;

OY          29 CACGTCATTATCCCAACTTCCCAGGGGA 55  
             | ||||| ||||| |||||  
OB          28 CCCCATACTTCCACAGCCCCCAGGGGA 2

RESULT 19  
Sequence 323, Application US/0907613  
Publication No. US20030027145A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Flvaroff, Ellen  
APPLICANT: Gong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Goddard, A.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillen, Kenneth J.  
APPLICANT: Kijavlin, Iwar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William E.

Query Match      13.2%    Score 15.8; DB 9; Length 45;  
Best Local Similarity     74.1%; Pred. No. 2.2e+04;  
Matches        20; Conservative    0; Mismatches        7; Indels            0; Gaps            0;

OY          29 CACGTCATTATCCCAACTTCCCAGGGGA 55  
             | ||||| ||||| |||||  
OB          28 CCCCATACTTCCACAGCCCCCAGGGGA 2

RESULT 20  
Sequence 323, Application US/0907942  
Publication No. US20030027146A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Flvaroff, Ellen  
APPLICANT: Gong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottfredsson, Mary E.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillen, Kenneth J.  
APPLICANT: Kijavlin, Iwar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tamas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William E.

JS-09-904-011-323



```

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-01-20
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 323
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
; US-09-907-841-323

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Query Match 13.24; Score 15.8; DB 9; Length 45;
Best Local Similarity 74.18; Pred. No. 2.2e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy 29 CACCTATTATCCCACTCCAGAGGGA 55
Db 28 CCCCACTATCCCACTCCAGAGGGA 2

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RESULT 16
US-09-904-011-323/C
; Sequence 323; Application US/0904011
; Publication No. US20030003536A1
; GENERAL INFORMATION:

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; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/25214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 323
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe

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3 PRIOR FILING DATE: 1999-07-07
4 PRIOR APPLICATION NUMBER: US 60/145,698
5 PRIOR FILING DATE: 1999-07-26
6 PRIOR APPLICATION NUMBER: US 60/146,222
7 PRIOR FILING DATE: 1999-07-28
8 PRIOR APPLICATION NUMBER: PCT/US99/20594
9 PRIOR FILING DATE: 1999-09-08
10 PRIOR APPLICATION NUMBER: PCT/US99/20944
11 PRIOR FILING DATE: 1999-09-13
12 PRIOR APPLICATION NUMBER: PCT/US99/21090
13 PRIOR FILING DATE: 1999-09-15
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15 PRIOR FILING DATE: 1999-09-15
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17 PRIOR FILING DATE: 1999-10-05
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33 PRIOR FILING DATE: 2000-01-05
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36 LENGTH: 45
37 TYPE: DNA
38 ORGANISM: Artificial Sequence
39 FEATURE:
40 OTHER INFORMATION: Synthetic Oligonucleotide
41 US-09-902-953-323

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APPLICANT:	Mather, Jennie P.
APPLICANT:	Pan, James
APPLICANT:	Paoni, Nicholas F.
APPLICANT:	Roy, Margaret Ann
APPLICANT:	Stewart, Timothy A.
APPLICANT:	Tunas, Daniel
APPLICANT:	Williams, P. Mickey
APPLICANT:	Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same	
FILE REFERENCE: 10466-14	
CURRENT APPLICATION NUMBER: US/09/907 824	
PRIOR FILING DATE: 2001-07-17	
PRIOR APPLICATION NUMBER: 09/665,350	
PRIOR FILING DATE: 2000-09-18	
PRIOR APPLICATION NUMBER: PCT/US00/04114	
PRIOR FILING DATE: 2000-02-22	
PRIOR APPLICATION NUMBER: US 60/143,018	
PRIOR FILING DATE: 1999-07-07	
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PRIOR FILING DATE: 1999-11-30	
PRIOR APPLICATION NUMBER: PCT/US99/28164	
PRIOR FILING DATE: 1999-12-07	
PRIOR APPLICATION NUMBER: PCT/US99/28165	
PRIOR FILING DATE: 1999-12-02	
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PRIOR APPLICATION NUMBER: PCT/US00/00119	
PRIOR FILING DATE: 2000-01-05	
NUMBER OF SEQ ID NOS: 423	
SEQ ID NO 323	
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TYPE: DNA	
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OTHER INFORMATION: Synthetic Oligonucleotide Probe	
US-09-907-824-323	



NAME/KEY: misc.feature  
LOCATION: (1)...(4)  
OTHER INFORMATION: phosphothioate 3'-Internucleotide linkage  
NAME/KEY: misc.feature  
LOCATION: (17)...(17)  
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NAME/KEY: misc.feature  
LOCATION: (19)...(19)  
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NAME/KEY: misc.feature  
LOCATION: (35)...(35)  
OTHER INFORMATION: n stands for inverted deoxybasic derivative  
US-09-848-75A-9596

Query Match 13.5% Score 16.2; DB 9; Length 36;  
Best Local Similarity 72.4%; Pred. No. 1.4e+04;  
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 35 CATTGACTCAGGAGGAGGATTCAGGG 7

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Sequence 378, Application US/09765272  
Patent No. US20020061545A1  
GENERAL INFORMATION:  
APPLICANT: Chol et. al.  
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines  
NUMBER OF SEQUENCES: 452  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
OPERATING SYSTEM: HP Vectra 486/33  
SOFTWARE: MSDOS version 6.2  
CURRENT APPLICATION DATA:  
FILING DATE: 22-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIORITY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB340P2  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 378:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 378:

US-09-765-272-378  
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Best Local Similarity 72.4%; Pred. No. 1.4e+04;  
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Db 2 AGTAAGCTTCGAGACCCATTCGCAATT 30

RESULT 10  
US-10-079-616-14/c  
Sequence 14, Application US/10079616  
Patent No. US20020107366A1  
GENERAL INFORMATION:  
APPLICANT: IMAMURA, Takayuki  
MAEDA, Hiroaki  
FUJIYASU, Takeshi  
IMAGAMA, Yoshitaka  
TOKIYOSHI, Sachio  
TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 22-Feb-2002  
CLASSIFICATION: <Unknown>  
PRIORITY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: IMAMURA-1  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-10-079-616-14  
Query Match 13.3% Score 16; DB 12; Length 44;  
Best Local Similarity 62.5%; Pred. No. 1.8e+04;  
Matches 25; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Oy 32 CTCATTATCCCATCCAGGAGGATTCAGGGTTCCAGCG 71  
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RESULT 11  
US-09-801-274-259/c  
Sequence 259, Application US/09801274  
Patent No. US20020032319A1  
GENERAL INFORMATION:  
APPLICANT: Cargill, Michele  
APPLICANT: Ireland, James S.  
APPLICANT: Lander, Eric S.  
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
FILE REFERENCE: 2825.2009-001







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GenCore version 5.1.6
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Run on:         June 17, 2003, 21:37:31 : Search time 121 Seconds
                                     (without alignments)
                                     1436.093 Million cell updates/sec

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Scoring table:  IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:       1029858 seqs, 72403093 residues      824824

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 8
Maximum DB Seq length: 50

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2 17.8 14.8 38 10 US-09-903-412-23      Sequence 23, App
3 17.8 14.8 38 10 US-09-096-749A-23      Sequence 23, App
4 17.8 14.8 38 10 US-09-951-401-35      Sequence 35, App
5 17.8 14.8 38 10 US-09-922-101-35      Sequence 35, App
6 17.8 14.8 38 10 US-09-922-101-35      Sequence 35, App
7 16.8 14.0 31 10 US-09-765-272-323      Sequence 323, App
8 16.2 13.5 36 9 US-09-848-754A-9596      Sequence 9596, App
9 16.2 13.5 37 10 US-09-765-272-378      Sequence 378, App
10 16.2 13.5 44 12 US-10-079-616-14      Sequence 14, App
11 15.8 13.2 45 9 US-09-905-291A-123      Sequence 259, App
12 15.8 13.2 45 9 US-09-902-853-323      Sequence 323, App
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GenCore version 5.1.6  
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score greater than or equal to the score of the result being printed,  
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# SUMMARIES

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C 6	17.8	14.8	38	6	AR159530 Sequence
C 7	17.8	14.8	38	6	AR159529 Sequence
C 8	17.8	14.8	38	6	AR159528 Sequence
C 9	17.8	14.8	38	6	AR159527 Sequence
C 10	17.8	14.8	38	6	AR159526 Sequence
C 11	17.8	14.8	38	6	AR159525 Sequence
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C 33	17.8	14.8	38	6	AR159503 Sequence
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C 39	17.8	14.8	38	6	AR159497 Sequence
C 40	17.8	14.8	38	6	AR159496 Sequence
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C 44	17.8	14.8	38	6	AR159492 Sequence
C 45	17.8	14.8	38	6	AR159491 Sequence
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C 59	17.8	14.8	38	6	AR159477 Sequence
C 60	17.8	14.8	38	6	AR159476 Sequence
C 61	17.8	14.8	38	6	AR159475 Sequence
C 62	17.8	14.8	38	6	AR159474 Sequence
C 63	17.8	14.8	38	6	AR159473 Sequence
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70	15.6	13.0	49	6	ARI628	Sequence 5	143	14.8	12.3	30	6	192350	Sequence 7
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c 72	15.6	13.0	50	6	AX098266	Sequence	145	14.8	12.3	31	6	A46551	Sequence 7
c 73	15.6	13.0	50	10	S60243	IQK DJ c10	146	14.8	12.3	31	6	A46551	Sequence 6
c 74	15.4	12.8	30	6	AX343940	Sequence	c 147	14.8	12.3	31	6	AX248499	Sequence 6
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76	15.4	12.8	39	6	ARO36028	Sequence	c 149	14.8	12.3	33	6	S4521353	Sequence
77	15.4	12.8	39	6	ARI26771	Sequence	c 150	14.8	12.3	37	6	ARI42293	Sequence 21
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79	15.4	12.8	39	6	AX006840	Sequence	c 152	14.8	12.3	37	6	132747	Sequence 21
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c 96	15.4	12.8	50	6	147216	Sequence 18	c 169	14.8	12.3	47	6	AX397630	Sequence
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c 98	15.2	12.7	20	6	AX487275	Sequence	171	14.8	12.3	48	11	G34982	DFFRX human
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c 100	15.2	12.7	28	6	ARI7155	Sequence	173	14.8	12.3	49	6	ARI45009	Sequence
c 101	15.2	12.7	35	6	ARI20558	Sequence 15	174	14.8	12.3	49	6	E59830	GMP synthas
c 102	15.2	12.7	36	6	ARI7163	Sequence 23	175	14.8	12.3	49	6	I92353	Sequence 5
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c 106	15.2	12.7	37	6	AX034570	Sequence	179	14.6	12.2	27	9	HUMTCIGC8A	Sequence 5
c 107	15.2	12.7	38	6	AX078461	Sequence	c 180	14.6	12.2	30	6	AX5831	Sequence 4
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c 111	15.2	12.7	40	6	ARI7178	Sequence 13	c 184	14.6	12.2	32	6	ARO34836	Sequence
c 112	15.2	12.7	40	6	ARI22572	Sequence	c 185	14.6	12.2	32	6	ARO34837	Sequence
c 113	15.2	12.7	40	6	ARI206383	Sequence	c 186	14.6	12.2	32	6	ARO33078	Sequence
c 114	15.2	12.7	41	6	141103	Sequence 6	c 187	14.6	12.2	32	6	ARO33079	Sequence
c 115	15.2	12.7	41	6	AX040471	Sequence	c 188	14.6	12.2	32	6	ARO33080	Sequence
c 116	15.2	12.7	42	6	ARO56492	Sequence	c 189	14.6	12.2	33	6	A67210	Sequence 1
c 117	15.2	12.7	42	6	AX027760	Sequence	c 190	14.6	12.2	33	6	ARO80690	Sequence
c 118	15.2	12.7	45	6	ARI7117	Sequence 27	c 191	14.6	12.2	33	6	ARO80592	Sequence
c 119	15.2	12.7	45	6	ARO77600	Sequence	c 192	14.6	12.2	33	6	AX113720	Sequence
c 120	15.2	12.7	45	6	AR206371	Sequence	c 193	14.6	12.2	36	6	AX395682	Sequence
c 121	15.2	12.7	48	6	ARO09909	Sequence	c 194	14.6	12.2	37	6	ARO09605	Sequence
c 122	15.2	12.7	48	6	AX068156	Sequence	c 195	14.6	12.2	37	6	ARO09606	Sequence
c 123	15.2	12.7	49	6	AX103399	Sequence	c 196	14.6	12.2	37	6	ARO316065	Sequence
c 124	15.2	12.7	50	6	AX075351	Sequence	c 197	14.6	12.2	37	6	ARO316066	Sequence
c 125	15.2	12.7	50	6	AX158999	Sequence	c 198	14.6	12.2	37	6	ARI60110	Sequence
c 126	15.2	12.7	35	6	AX3009	Sequence 1	c 199	14.6	12.2	37	6	121674	Sequence 2
c 127	15.2	12.7	35	6	AX3010	Sequence 2	c 200	14.6	12.2	37	6	121675	Sequence 2
c 128	15.2	12.7	35	6	A63763	Sequence 27							
c 129	15.2	12.7	35	6	111524	Sequence 1							
c 130	15.2	12.7	35	6	111525	Sequence 2							
c 131	15.2	12.7	35	6	AX008381	Sequence							
c 132	15.2	12.7	36	6	AX395685	Sequence							
c 133	15.2	12.7	38	6	ARI82872	Sequence							
c 134	15.2	12.7	42	6	ARI3593	Sequence 11							
c 135	15.2	12.7	42	6	ARO01432	Sequence							
c 136	15.2	12.7	43	6	ARI1806	Sequence							
c 137	15.2	12.7	45	6	ECOPHOA3	J01661 E.coli phoA							
c 138	15.2	12.7	49	6	ARI1803	J01803 Trp-5, 12/1							

RESULT 1

ARI69537

LOCUS

DEFINITION

ACCESSION

VERSION

ARI69537

Sequence 35

from patent US 6291173.

ARI69537

ARI69537.1

GI:17907405

linear

38 bp

DNA

PAT 17-DEC-2001

ALIGNMENTS

## ALIGNMENTS

RESULT 1	ARI69537	38 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	Sequence 35 from patent US 6291173				
DEFINITION	Sequence 35 from patent US 6291173				
ACCESSION	ARI69537				
VERSION	ARI69537.1				GI:17907405



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variation
BASE COUNT      9 a      9 c      11 g      17 t      1 others
ORIGIN
/organism="Homo sapiens"
/db_xref="taxon:9606"
24
/note="99-26413-307 : polymorphic base A or T"
17 t      1 others
Query Match      14.7%      Score 17.6;      DB 6;      Length 47;
Best Local Similarity 67.6%;      Pred. No. 2.4e+05;
Matches 23;      Conservative 1;      Mismatches 10;      Indels 0;      Gaps 0;

QY      22 TAACCCACACCTCATTATCCCACTCCAGAGGGA 55
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DB      35 TAACCCACACGACACATCTTCAGCACAGAGGGA 2

RESULT 6
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LOCUS      AXI65107
DEFINITION      Sequence 302 from Patent WO0138586.
ACCESSION      AXI65107
VERSION      AXI65107.1
KEYWORDS      GI:14545936
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 50)
AUTHORS      Shimkets,R.A. and Leach,M.
TITLE      Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL      Patent: WO 0138586-A 302 31-MAY-2001;
Curagen Corporation (US)
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
25..26
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25..26
/note="Nucleotide deleted between bases 25 and 26"
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Query Match      14.5%      Score 17.4;      DB 6;      Length 50;
Best Local Similarity 68.6%;      Pred. No. 2.8e+05;
Matches 24;      Conservative 0;      Mismatches 11;      Indels 0;      Gaps 0;

QY      54 GATTCAGGGTTCACAGCGTCTCGAAATGATCGA 88
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DB      43 GTTCACTGATACCTGCTTTCTGAAATGATCGA 9

RESULT 7
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LOCUS      AXI6709
DEFINITION      Sequence 7 from Patent WO9838299.
ACCESSION      AXI6709
VERSION      AXI6709.1
KEYWORDS      GI:6735851
SOURCE      unidentified.
ORGANISM      unidentified.
REFERENCE      1 (bases 1 to 35)
AUTHORS      Sharon,G.
TITLE      SINGLE STEP ASSEMBLY OF MULTIPLE DNA FRAGMENTS
JOURNAL      Patent: WO 9838299-A 7 03-SEP-1998;
SHARON GIL (IL); GESHER ISRAEL ADVANCED BIOTECS (IL)
FEATURES
Location/Qualifiers
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Query Match      14.3%      Score 17.2;      DB 6;      Length 35;
Best Local Similarity 73.3%;      Pred. No. 3.2e+05;
Matches 22;      Conservative 0;      Mismatches 8;      Indels 0;      Gaps 0;

QY      89 TTGGCTTCATAGCTGCTGAATTCAGTTT 118
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DB      31 TTAGCTTCCTAGCTCCTGATTCATGTT 2

RESULT 8
AXI7123/c
LOCUS      AXI7123
DEFINITION      Sequence 33 from Patent WO9838298.
ACCESSION      AXI7123
VERSION      AXI7123.1
KEYWORDS      GI:6735895
SOURCE      unidentified.
ORGANISM      unidentified.
REFERENCE      1 (bases 1 to 35)
AUTHORS      Sharon,G.
TITLE      METHOD FOR ASSEMBLY OF MULTIPLE DNA FRAGMENTS
JOURNAL      Patent: WO 9838298-A 33 03-SEP-1998;
SHARON GIL (IL); GESHER ISRAEL ADVANCED BIOTECS (IL)
FEATURES
Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT      17 a      4 c      9 g      5 t
ORIGIN
Query Match      14.3%      Score 17.2;      DB 6;      Length 35;
Best Local Similarity 73.3%;      Pred. No. 3.2e+05;
Matches 22;      Conservative 0;      Mismatches 8;      Indels 0;      Gaps 0;

QY      89 TTGGCTTCATAGCTGCTGAATTCAGTTT 118
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DB      31 TTAGCTTCCTAGCTCCTGATTCATGTT 2

RESULT 9
AXI7147/c
LOCUS      AXI7147
DEFINITION      Sequence 7 from Patent WO9838297.
ACCESSION      AXI7147
VERSION      AXI7147.1
KEYWORDS      GI:6735919
SOURCE      unidentified.
ORGANISM      unidentified.
REFERENCE      1 (bases 1 to 35)
AUTHORS      Sharon,G.
TITLE      SINGLE STEP ASSEMBLY OF MULTIPLE DNA FRAGMENTS
JOURNAL      Patent: WO 9838297-A 7 03-SEP-1998;
SHARON GIL (IL); GESHER ISRAEL ADVANCED BIOTECS (IL)
FEATURES
Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT      17 a      4 c      9 g      5 t
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Query Match      14.3%      Score 17.2;      DB 6;      Length 35;
Best Local Similarity 73.3%;      Pred. No. 3.2e+05;
Matches 22;      Conservative 0;      Mismatches 8;      Indels 0;      Gaps 0;

QY      89 TTGGCTTCATAGCTGCTGAATTCAGTTT 118
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DB      31 TTAGCTTCCTAGCTCCTGATTCATGTT 2

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RESULT 10  
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DEFINITION Sequence 2 from Patent W09838296.  
ACCESSION A87167  
VERSION A87167.1 GI:6735939  
KEYWORDS  
SOURCE unidentified.  
ORGANISM  
REFERENCE 1 (bases 1 to 35)  
TITLE METHOD FOR SIMULTANEOUS LIGATION OF MULTIPLE DNA FRAGMENTS  
JOURNAL SHARON GIL (IL); GESHER ISRAEL ADVANCED BIOTECS (IL)  
FEATURES  
Location/Qualifiers  
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/db\_xref="taxon:32644"  
BASE COUNT 17 a 4 c 9 g 5 t  
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Best Local Similarity 73.3%; Pred. No. 3.2e+05;  
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
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Db 31 TTAGCTTCTTAGCTCTGCTGATTCATGTT 2  
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A87167/c  
LOCUS A87167 35 bp DNA PAT 20-JUN-2002  
DEFINITION Sequence 33 from patent US 6372429.  
ACCESSION A87167  
VERSION A87167.1 GI:21504961  
KEYWORDS  
SOURCE Unknown.  
ORGANISM  
REFERENCE 1 (bases 1 to 35)  
TITLE Method for assembly of multiple DNA fragments  
JOURNAL SHARON G.  
AUTHORS Sharon G.  
TITLE Method for assembly of multiple DNA fragments  
JOURNAL Patent: US 6372429-A 33 16-APR-2002;  
FEATURES  
Location/Qualifiers  
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/organism="unknown"  
BASE COUNT 17 a 4 c 9 g 5 t  
ORIGIN  
Query Match 14.3% Score 17.2; DB 6; Length 35;  
Best Local Similarity 73.3%; Pred. No. 3.2e+05;  
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
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RESULT 12  
A87115/c  
LOCUS A87115 37 bp DNA PAT 22-JAN-2000  
DEFINITION Sequence 25 from Patent W09838298.  
ACCESSION A87115  
VERSION A87115.1 GI:6735887  
KEYWORDS  
SOURCE unidentified.  
ORGANISM  
REFERENCE 1 (bases 1 to 37)  
TITLE  
AUTHORS Sharon G.

METHOD FOR ASSEMBLY OF MULTIPLE DNA FRAGMENTS  
PATENT: WO 9838298-A 25 03-SEP-1998;  
SHARON GIL (IL); GESHER ISRAEL ADVANCED BIOTECS (IL)  
FEATURES  
Location/Qualifiers  
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/db\_xref="taxon:32644"  
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Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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Db 32 TTAGCTTCTTAGCTCTGATTCAT 11  
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RESULT 13  
A87115/c  
LOCUS A87115 45 bp DNA PAT 31-AUG-2000  
DEFINITION Sequence 9 from patent US 5969119.  
ACCESSION A87115  
VERSION A87115.1 GI:10007629  
KEYWORDS  
SOURCE Unknown.  
ORGANISM  
REFERENCE 1 (bases 1 to 45)  
TITLE DNA sequencing by parallel oligonucleotide extensions  
JOURNAL Patent: US 5969119-A 9 19-OCT-1999;  
FEATURES  
Location/Qualifiers  
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Matches 25; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 11 AGTGACCTCTTACCCACACCTCATTATCCCACTCC 48



ORGANISM Unknown.  
 UNCLASSIFIED.  
 REFERENCE 1 (bases 1 to 37)  
 AUTHORS Macevicz, S.C.  
 TITLE DNA sequencing by parallel oligonucleotide extensions  
 JOURNAL Patent: US 5750341-A 1 12-MAY-1998;  
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BASE COUNT 0 a 25 c 0 g 12 t  
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 Matches 23; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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 DEFINITION Sequence 1 from patent US 5969119.  
 ACCESSION ARI080892  
 VERSION ARI080892.1 GI:10007621  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 37)  
 AUTHORS Macevicz, S.C.  
 TITLE DNA sequencing by parallel oligonucleotide extensions  
 JOURNAL Patent: US 5969119-A 1 19-OCT-1999;  
 FEATURES Location/Qualifiers  
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BASE COUNT 0 a 25 c 0 g 12 t  
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Query Match 14.2% Score 17; DB 6; Length 37;  
 Best Local Similarity 69.7% Pred. No. 3.8e+05;  
 Matches 23; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 16 CCTCTTACCCACACCTCATTTATCCCACTCC 48  
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 Db 2 CTCTCCCTCCCTCTCTCTCTCTCTCTCTCTCC 34

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 LOCUS ARI73722  
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 ACCESSION ARI73722  
 VERSION ARI73722.1 GI:17914042  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 37)  
 AUTHORS Macevicz, S.C.  
 TITLE DNA sequencing by parallel oligonucleotide extensions  
 JOURNAL Patent: US 6306597-A 1 23-OCT-2000;  
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BASE COUNT 0 a 25 c 0 g 12 t  
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Query Match 14.2% Score 17; DB 6; Length 37;  
 Best Local Similarity 69.7% Pred. No. 3.8e+05;  
 Matches 23; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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 Db 2 CTCTCCCTCCCTCTCTCTCTCTCTCTCTCTCC 34

## RESULT 22

ARI20447/c  
 LOCUS ARI20447/c  
 DEFINITION Sequence 323 from patent US 6159469.  
 ACCESSION ARI20447  
 VERSION ARI20447.1 GI:14104023  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 31)  
 AUTHORS Choi, G.H., Kunsch, C.A., Barash, S.C., Dillon, P.J., Dougherty, B., Fannon, M.R., and Rosen, C.A.  
 TITLE Streptococcus pneumoniae antigens and vaccines  
 JOURNAL Patent: US 6159469-A 323 12-DEC-2000;  
 FEATURES Location/Qualifiers  
 1..31  
 source /organism="unknown"

BASE COUNT 10 a 9 c 7 g 5 t  
 ORIGIN

Query Match 14.0% Score 16.8; DB 6; Length 31;  
 Best Local Similarity 75.0% Pred. No. 4.4e-05;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 71 GTTCTCAAAATGATGATGCTTGGTCCCA 98  
 11111111 111 11111 1111  
 Db 31 GTTCTCAAAATGATGATGCTTGGTCCCA 4

## RESULT 23

AX378356/c  
 LOCUS AX378356  
 DEFINITION Sequence 145 from Patent WO0206525.  
 ACCESSION AX378356  
 VERSION AX378356.1 GI:19574206  
 KEYWORDS  
 SOURCE Human.  
 ORGANISM Homo sapiens

REFERENCE 1  
 AUTHORS Cohen, D., Blumenfeld, M., Chumakov, I., Abderrahim, H. and Bihain, B.  
 TITLE Obesity associated biallelic marker maps  
 JOURNAL Patent: WO 0206525-A 145 24-JAN-2002;  
 FEATURES Location/Qualifiers  
 1..47  
 source /organism="Homo sapiens"

variation /db\_xref="taxon:9606"  
 24  
 BASE COUNT 17 a 9 c 9 g 11 t 1 others

Query Match 13.8% Score 16.6; DB 6; Length 47;  
 Best Local Similarity 61.0% Pred. No. 5.4e+05;  
 Matches 25; Conservative 1; Mismatches 15; Indels 0; Gaps 0;

Oy 63 GTTCAGCGTCTCTGAAATGATGCTTGGTCCATAGCT 103  
 11111111 11111111 11111111  
 Db 46 GTTCAGCGTCTCTGAAATGATGCTTGGTCCATAGCT 6

## RESULT 24

AX004493  
 LOCUS AX004493  
 DEFINITION Sequence 33 from patent US 6159469.  
 ACCESSION AX004493  
 VERSION AX004493.1 GI:14104023  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 33)  
 AUTHORS Choi, G.H., Kunsch, C.A., Barash, S.C., Dillon, P.J., Dougherty, B., Fannon, M.R., and Rosen, C.A.  
 TITLE Streptococcus pneumoniae antigens and vaccines  
 JOURNAL Patent: US 6159469-A 333 12-DEC-2000;  
 FEATURES Location/Qualifiers  
 1..33  
 source /organism="unknown"

BASE COUNT 10 a 9 c 7 g 5 t  
 ORIGIN

Query Match 14.0% Score 16.8; DB 6; Length 31;  
 Best Local Similarity 75.0% Pred. No. 4.4e-05;  
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

DEFINITION Sequence 18 from Patent WO9916892.

ACCESSION AX004493

VERSION AX004493.1 GI:5927947

KEYWORDS synthetic construct.

SOURCE synthetic construct.

ORGANISM artificial construct.

REFERENCE 1 (bases 1 to 33)

AUTHORS Duffas, W.P. and Bradley, A.J.

TITLE Bovine herpesvirus 2 (bHV-2) based vector and its uses

JOURNAL Patent: WO 9916892-A 18 08-APR-1999;

DUFFAS W P H (GB); UNIV BRISTOL (GB)

FEATURES

source 1..33

/organism="synthetic construct"

/db\_xref="taxon:32630"

/note="Oligonucleotide primer"

BASE COUNT 9 a 13 c 6 g 5 t

ORIGIN

Query Match 13.7% Score 16.4; DB 6; Length 33;

Best Local Similarity 76.9% Pred. No. 6.2e+05;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCGATGCCATAGTACCCCTCAACC 26

DB 6 TCGATCCAGAGTACCCACCTCACC 31

RESULT 25

AX078734

LOCUS AX078734

DEFINITION Sequence 30 from Patent WO0107573.

ACCESSION AX078734

VERSION AX078734.1 GI:13158358

KEYWORDS synthetic construct.

SOURCE synthetic construct.

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 38)

AUTHORS Hauer, B., Schmid, R.D. and Schwaneberg, U.

TITLE Electron donor system for enzymes and its use for the biochemical

JOURNAL conversion of substrates

Patent: WO 0107573-A 30 01-FEB-2001;

BASF AKTIENGESellschaft (DE)

FEATURES

source 1..38

/organism="synthetic construct"

/db\_xref="taxon:32630"

/note="Oligonucleotide fuer Tag am C-Terminus"

BASE COUNT 6 a 16 c 8 g 8 t

ORIGIN

Query Match

Best Local Similarity 13.7% Score 16.4; DB 6; Length 38;

Matches 23; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 8 CATAGTACCCTCTAACCCACACCTCATATCC 41

DB 5 CAGCGTGAGACCCACCCACACCTCTTTGCC 38

RESULT 26

A79785/c

LOCUS A79785

DEFINITION Sequence 12 from Patent EP077545.

ACCESSION A79785

VERSION A79785.1 GI:6092704

KEYWORDS unidentified.

SOURCE unidentified.

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 42)

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

RESULT 27

AX018115/c

LOCUS AX018115

DEFINITION Sequence 12 from patent US 5780449.

ACCESSION AX018115

VERSION AX018115.1 GI:3973718

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

RESULT 28

HUMIGHACH/c

LOCUS HUMIGHACH

DEFINITION Human Ig rearranged mu-chain mRNA V-region, partial cds (from clone

FS-C).

ACCESSION L07018

VERSION L07018.1 GI:184995

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TOI.N.J.D.

Bracht, F. and Schroer, K.P.

CATHEPSIN G-INHIBITING APTAMERS

Patent: EP 0775745-A 12 28-MAY-1997;

CRINOS INDUSTRIA FARMACO (IT)

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

RESULT 29

AX018115/c

LOCUS AX018115

DEFINITION Sequence 12 from patent US 5780449.

ACCESSION AX018115

VERSION AX018115.1 GI:3973718

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

RESULT 30

HUMIGHACH/c

LOCUS HUMIGHACH

DEFINITION Human Ig rearranged mu-chain mRNA V-region, partial cds (from clone

FS-C).

ACCESSION L07018

VERSION L07018.1 GI:184995

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TOI.N.J.D.

Bracht, F. and Schroer, K.P.

CATHEPSIN G-INHIBITING APTAMERS

Patent: EP 0775745-A 12 28-MAY-1997;

CRINOS INDUSTRIA FARMACO (IT)

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

RESULT 31

AX018115/c

LOCUS AX018115

DEFINITION Sequence 12 from patent US 5780449.

ACCESSION AX018115

VERSION AX018115.1 GI:3973718

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

RESULT 32

HUMIGHACH/c

LOCUS HUMIGHACH

DEFINITION Human Ig rearranged mu-chain mRNA V-region, partial cds (from clone

FS-C).

ACCESSION L07018

VERSION L07018.1 GI:184995

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TOI.N.J.D.

Bracht, F. and Schroer, K.P.

CATHEPSIN G-INHIBITING APTAMERS

Patent: EP 0775745-A 12 28-MAY-1997;

CRINOS INDUSTRIA FARMACO (IT)

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

RESULT 33

AX018115/c

LOCUS AX018115

DEFINITION Sequence 12 from patent US 5780449.

ACCESSION AX018115

VERSION AX018115.1 GI:3973718

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

RESULT 34

HUMIGHACH/c

LOCUS HUMIGHACH

DEFINITION Human Ig rearranged mu-chain mRNA V-region, partial cds (from clone

FS-C).

ACCESSION L07018

VERSION L07018.1 GI:184995

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TOI.N.J.D.

Bracht, F. and Schroer, K.P.

CATHEPSIN G-INHIBITING APTAMERS

Patent: EP 0775745-A 12 28-MAY-1997;

CRINOS INDUSTRIA FARMACO (IT)

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

RESULT 35

AX018115/c

LOCUS AX018115

DEFIN





QY 60 GGGTTCAGCGCTTCCTGAAATGATCGAT 89  
 DB 2 GGGATCGATCGATCGGGAATGATCGAT 31  
  
 RESULT 33  
 AX300707/c  
 LOCUS AX300707 34 bp DNA linear PAT 30-NOV-2001  
 DEFINITION Sequence 7 from patent WO0185965.  
 ACCESSION AX300707  
 VERSION AX300707.1 GI:17382010  
 KEYWORDS synthetic construct.  
 ORGANISM synthetic construct  
 FEATURES Location/Qualifiers  
 1..34  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="Primer"  
 BASE COUNT 13 a 4 c 11 g 6 t  
 ORIGIN  
  
 Query Match 13.5% Score 16.2; DB 6; Length 34;  
 Best Local Similarity 85.7%; Pred. No. 7.4e+05;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 89 TTGGCTTCATAGCTGCTGAA 109  
 DB 23 TTAGCTTCCTAGCTCTGAA 9  
  
 RESULT 34  
 ARI20502  
 LOCUS ARI20502 37 bp DNA linear PAT 16-MAY-2001  
 DEFINITION Sequence 378 from patent US 6159469.  
 ACCESSION ARI20502  
 VERSION ARI20502.1 GI:14104078  
 KEYWORDS Streptococcus pneumoniae antigens and vaccines  
 ORGANISM Streptococcus pneumoniae  
 REFERENCE 1 (bases 1 to 37)  
 AUTHORS Choi, G.H., Kunsch, C.A., Barash, S.C., Dillon, P.J., Dougherty, B., Fannon, M.R. and Rosen, C.A.  
 TITLE Streptococcus pneumoniae antigens and vaccines  
 JOURNAL Patent: US 6159469-A 378 12-DEC-2000;  
 FEATURES Location/Qualifiers  
 1..37  
 /organism="unknown"  
 /db\_xref="taxon:32630"  
 /note="Primer"  
 BASE COUNT 10 a 11 c 6 g 10 t  
 ORIGIN  
  
 Query Match 13.5% Score 16.2; DB 6; Length 37;  
 Best Local Similarity 72.4%; Pred. No. 7.4e+05;  
 Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
 QY 11 AGTGACCTCTTACCCACACCTCATAT 39  
 DB 2 AGTAAGCTTCGGAACCCATTCGCCATTAT 30  
  
 RESULT 35  
 A12459/c  
 LOCUS A12459 38 bp mRNA linear PAT 05-JAN-1994  
 DEFINITION Partial CAT mRNA from pull 102.  
 ACCESSION A12459  
 VERSION A12459.1 GI:491369

KEYWORDS synthetic construct.  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct.  
 FEATURES Location/Qualifiers  
 1..38  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 BASE COUNT 13 a 5 c 12 g 8 t  
 ORIGIN  
  
 Query Match 13.5% Score 16.2; DB 6; Length 38;  
 Best Local Similarity 85.7%; Pred. No. 7.4e+05;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 89 TTGGCTTCATAGCTGCTGAA 109  
 DB 33 TTAGCTTCCTAGCTCTGAA 13  
  
 RESULT 36  
 ARI04333/c  
 LOCUS ARI04333 39 bp DNA linear PAT 14-FEB-2001  
 DEFINITION Sequence 12 from patent US 6093554.  
 ACCESSION ARI04333  
 VERSION ARI04333.1 GI:12817041  
 KEYWORDS Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 39)  
 AUTHORS Haute, E., Van, A., Aneloot, P., Lafonteyne, J. De, and Fiers, W.  
 TITLE Genetic manipulations with recombinant DNA virus comprising sequences derived from RNA virus  
 JOURNAL Patent: US 6093554-A 12 25-JUL-2000;  
 FEATURES Location/Qualifiers  
 1..39  
 /organism="unknown"  
 /db\_xref="taxon:32630"  
 /note="Primer"  
 BASE COUNT 14 a 6 c 10 g 9 t  
 ORIGIN  
  
 Query Match 13.5% Score 16.2; DB 6; Length 39;  
 Best Local Similarity 85.7%; Pred. No. 7.4e+05;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 89 TTGGCTTCATAGCTGCTGAA 109  
 DB 35 TTAGCTTCCTAGCTCTGAA 15  
  
 RESULT 37  
 ARI37620/c  
 LOCUS ARI37620 39 bp DNA linear PAT 16-JUN-2001  
 DEFINITION Sequence 12 from patent US 6197542.  
 ACCESSION ARI37620  
 VERSION ARI37620.1 GI:14479129  
 KEYWORDS Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 39)  
 AUTHORS Van Haute, E., Aneloot, P., De Lafonteyne, J. and Fiers, W.  
 TITLE Genetic manipulations with recombinant DNA comprising sequences derived from RNA virus  
 JOURNAL Patent: US 6197542-A 12 06-MAR-2001;  
 FEATURES Location/Qualifiers  
 1..39  
 /organism="unknown"  
 /db\_xref="taxon:32630"  
 /note="Primer"  
 BASE COUNT 14 a 6 c 10 g 9 t  
 ORIGIN  
  
 Query Match 13.5% Score 16.2; DB 6; Length 39;  
 Best Local Similarity 85.7%; Pred. No. 7.4e+05;

Matches 18: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

Oy 89 TTGGCTTCCATAGCTGCTGAA 109  
Db 35 TTAGCTTCCCTAGCTGCTGAA 15

RESULT 38  
LOCUS ARI68699  
DEFINITION Sequence 6 from patent US 6287863.  
ACCESSION ARI68699  
VERSION ARI68699.1 GI:17904754  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 45)  
AUTHORS Hodgson,C.P.  
TITLE Method of transferring a DNA sequence to a cell in vitro  
JOURNAL Patent: US 6287863-A 6 11-SEP-2001;  
FEATURES  
source Location/Qualifiers  
1..45  
BASE COUNT 16 a 5 c 10 g 14 t  
ORIGIN

Query Match 13.5% Score 16.2; DB 6: Length 45;  
Best Local Similarity 64.9%; Pred. No. 7.5e+05;  
Matches 24: Conservative 0: Mismatches 13: Indels 0: Gaps 0:

Oy 55 ATTGAGGGTTCAGGCTTCCTGAAATGATCGATTG 91  
Db 6 ATTAAATTGATCTAGCATGATGACACAGATGATGATTC 42

RESULT 39  
LOCUS AR201856/c  
DEFINITION Sequence 71 from patent US 6361941.  
ACCESSION AR201856  
VERSION AR201856  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 45)  
AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.  
TITLE Catalytic nucleic acid-based diagnostic methods  
JOURNAL Patent: US 6361941-A 71 26-MAR-2002;  
FEATURES  
source Location/Qualifiers  
1..45  
BASE COUNT 13 a 9 c 15 g 7 t 1 others  
ORIGIN

Query Match 13.5% Score 16.2; DB 6: Length 45;  
Best Local Similarity 72.4%; Pred. No. 7.5e+05;  
Matches 21: Conservative 0: Mismatches 8: Indels 0: Gaps 0:

Oy 17 CCGCTCAACCCACACCTCATTCATCCAC 45  
Db 31 CCGCTCAACCCACACCTCATTCATCCAC 3

RESULT 40  
LOCUS E60008  
DEFINITION Ceramide-binding peptide.  
ACCESSION E60008  
VERSION E60008.1 GI:18622767  
KEYWORDS JP 2000319296-A/8.  
SOURCE Synthetic construct.

Matches 18: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

Oy 89 TTGGCTTCCATAGCTGCTGAA 109  
Db 35 TTAGCTTCCCTAGCTGCTGAA 15

RESULT 38  
LOCUS ARI68699  
DEFINITION Sequence 6 from patent US 6287863.  
ACCESSION ARI68699  
VERSION ARI68699.1 GI:17904754  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 45)  
AUTHORS Hodgson,C.P.  
TITLE Method of transferring a DNA sequence to a cell in vitro  
JOURNAL Patent: US 6287863-A 6 11-SEP-2001;  
FEATURES  
source Location/Qualifiers  
1..45  
BASE COUNT 16 a 5 c 10 g 14 t  
ORIGIN

Query Match 13.5% Score 16.2; DB 6: Length 45;  
Best Local Similarity 64.9%; Pred. No. 7.5e+05;  
Matches 24: Conservative 0: Mismatches 13: Indels 0: Gaps 0:

Oy 55 ATTGAGGGTTCAGGCTTCCTGAAATGATCGATTG 91  
Db 6 ATTAAATTGATCTAGCATGATGACACAGATGATGATTC 42

RESULT 39  
LOCUS AR201856/c  
DEFINITION Sequence 71 from patent US 6361941.  
ACCESSION AR201856  
VERSION AR201856  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 45)  
AUTHORS Todd,A.V., Fuery,C.J. and Cairns,M.J.  
TITLE Catalytic nucleic acid-based diagnostic methods  
JOURNAL Patent: US 6361941-A 71 26-MAR-2002;  
FEATURES  
source Location/Qualifiers  
1..45  
BASE COUNT 13 a 9 c 15 g 7 t 1 others  
ORIGIN

Query Match 13.5% Score 16.2; DB 6: Length 45;  
Best Local Similarity 72.4%; Pred. No. 7.5e+05;  
Matches 21: Conservative 0: Mismatches 8: Indels 0: Gaps 0:

Oy 17 CCGCTCAACCCACACCTCATTCATCCAC 45  
Db 31 CCGCTCAACCCACACCTCATTCATCCAC 3

RESULT 40  
LOCUS E60008  
DEFINITION Ceramide-binding peptide.  
ACCESSION E60008  
VERSION E60008.1 GI:18622767  
KEYWORDS JP 2000319296-A/8.  
SOURCE Synthetic construct.

ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 45)  
AUTHORS Ishikawa,M., Tanaka,Y., Ogino,K. and Taki,T.  
TITLE Ceramide-binding peptide  
JOURNAL Patent: JP 2000319296-A 8 21-NOV-2000;  
COMMENT OTSUKA PHARMACEUT CO LTD  
OS Artificial Sequence  
PN JP 2000319296-A/8  
PD 21-NOV-2000  
PF 10-MAY-1999 JP 1999128674  
PR MASARU ISHIKAWA,YOSHINOBU TANAKA,KOICHI OGINO,TAKAO TAKI PC  
C07K7/00  
CC  
FH Key location/Qualifiers  
FT source 1..45  
FT /organism="Artificial Sequence".  
FEATURES  
source Location/Qualifiers  
1..45  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
BASE COUNT 3 a 6 c 12 g 24 t  
ORIGIN

Query Match 13.5% Score 16.2; DB 6: Length 45;  
Best Local Similarity 64.9%; Pred. No. 7.5e+05;  
Matches 24: Conservative 0: Mismatches 13: Indels 0: Gaps 0:

Oy 82 TGATCGATGGCTTCATAGCTGCTGAATGCACTTT 118  
Db 9 TGATCGATGGCTTCATAGCTGCTGAATGCACTTT 45

RESULT 41  
LOCUS AX378360  
DEFINITION Sequence 149 from Patent WO0206525.  
ACCESSION AX378360  
VERSION AX378360.1 GI:15574210  
KEYWORDS human  
SOURCE human  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1  
AUTHORS Cohen,D., Blusenfeld,M., Chumakov,I., Abderrahim,H. and Bihain,B.  
TITLE Obesity associated cellular marker maps  
JOURNAL Patent: WO 0206525-A 149 24-JAN-2002;  
GENSET (FR)  
FEATURES  
source Location/Qualifiers  
1..47  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
variation 24  
/note="99-28342-137 : polymorphic base A or G"  
BASE COUNT 11 a 24 c 2 g 9 t 1 others  
ORIGIN

Query Match 13.5% Score 16.2; DB 6: Length 47;  
Best Local Similarity 64.9%; Pred. No. 7.6e+05;  
Matches 24: Conservative 0: Mismatches 13: Indels 0: Gaps 0:

Oy 15 ACCCTGCTTAACCCACACCTCATTCATCCACCTCAGA 52  
Db 3 ACCACCTTACCCACCTTCCTCCACACCTCAGA 39

RESULT 42  
LOCUS AX233387/c  
DEFINITION Sequence 30 from Patent WO0162788.  
ACCESSION AX233387

<b>AX233387.1</b>							
GI:15592721							
human.							
Homo sapiens							
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
1 (bases 1 to 50)							
Olaveson,M., Lench,N., Allen,M. and Tazi-Ahaini,R.U.							
Corneodesmosin based test and model for inflammatory disease							
Patent: WO 0162788.A 30 30-AUG-2001;							
Oxagen Limited (GB)							
Location/Qualifiers							
1..50							
/organism="Homo sapiens"							
/db_xref="taxon:9606"							
BASE COUNT 9 a 21 c 8 g 11 t 1 others							
ORIGIN							
Query Match 13.5%; Score 16.2; DB 6; Length 50:							
Best Local Similarity 57.4%; Pred. NO. 7.6e+05;							
Matches 27; Conservative 1; Mismatches 19; Indels 0; Gaps 0;							
Oy	48 CAGAGGATTTCAGGGTTCCCGCTTCTCCTGAATCATGTGCST 94       1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1						
Db	50 CAGCGATGGTAGCGTGAAACCGMGCTGCTGCAATGCTAGAACTGCT 4						
RESULT 43							
SYNRM3/C							
LOCUS SYNRM3/C							
DEFINITION Synthetic Brome mosaic virus (BMV) RNA 3' end/CAT gene from							
PB3CM42, partial cds.							
ACCESSION M19550							
VERSION M19550.1							
KEYWORDS GI:209273							
ORGANISM Brome mosaic virus and plasmid pB3CM42 RNA.							
SOURCE synthetic construct							
ARTIFACTS artificial sequences.							
1 (bases 1 to 50)							
French,R., Janda,M. and Ahlquist,P.G.							
Bacterial gene inserted in an engineered RNA virus: Efficient							
expression in monocotyledonous plant cells							
Science 231, 1294-1297 (1986)							
JOURNAL Science 231,							
Location/Qualifiers							
1..50							
/organism="synthetic construct"							
/db_xref="taxon:32630"							
CD5 10..>50							
/note="coat protein"							
/codon_start=1							
/trans_table=11							
/protein_id="AAA73637.1"							
/db_xref="GI:354572"							
/translation="MSRFSKAEAKW"							
BASE COUNT 19 a 5 c 13 g 13 t							
ORIGIN							
Query Match 13.5%; Score 16.2; DB 12; Length 50:							
Best Local Similarity 85.7%; Pred. NO. 7.6e+05;							
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;							
OY	89 TTGGCTTCCCATAGCTGCTGAA 109 						
Db	44 TTAGCTTCCTTAGCTCCTGAA 24						
RESULT 44							
DME42689/c							
LOCUS DME42689/c							
DEFINITION Drosophila melanogaster X Chromosomal sequences flanking P-lacW							
insertion, strain l(1)G0478.							
AJ426898							
AJ426898.1							
GI:18478119							

misc\_feature 9 a 12 c 16 g 13 t  
 BASE COUNT  
 ORIGIN  
 /note="Nucleotide deleted between bases 25 and 26  
 Accession number CG4009645"  
 /note="2 of 2 allelic variants (5585 is other entry)"

Query Match 13.3% Score 16; DB 6; Length 50;  
 Best Local Similarity 62.5%; Pred. No. 9e+05;  
 Matches 25; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 8 CAGAGCGGCGGCGATGTCGACATGACATGCGCCACCTC 47  
 DB 43 CAGAGCGGCGGCGATGTCGACATGACATGCGCCACCTC 4

RESULT 46  
 AX248180/c  
 LOCUS AX248180 31 bp DNA linear PAT 28-SEP-2001  
 DEFINITION Sequence 259 from Patent WO0166800.  
 ACCESSION AX248180  
 VERSION AX248180.1 GI:15862803  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 31)  
 AUTHORS Cargill, M., Ireland, J.S., and Lander, E.S.  
 TITLE Human single nucleotide polymorphisms  
 JOURNAL Patent: WO 0166800-A 259 13-SEP-2001;  
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

FEATURES  
 source  
 1. 31 Ism="Homo sapiens"  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 6 a 4 c 11 g 9 t 1 others  
 ORIGIN

Query Match 13.2% Score 15.8; DB 6; Length 31;  
 Best Local Similarity 69.0%; Pred. No. 1e+06;  
 Matches 20; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 27 CACAGCTCTATCCCTCCCTCCGAGGGA 55  
 DB 29 CACAGCTCTATCCCTCCCTCCGAGGGA 1

RESULT 47  
 AR012187/c  
 LOCUS AR012187 33 bp DNA linear PAT 04-DEC-1998  
 DEFINITION Sequence 3 from patent US 5763242.  
 ACCESSION AR012187  
 VERSION AR012187.1 GI:3970177  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.

REFERENCE 1 (bases 1 to 33)  
 AUTHORS Zhang, H. and Pomerantz, R.J.  
 TITLE Method for increasing transduction efficiency of recombinant retroviral vectors  
 JOURNAL Patent: US 5763242-A 3 09-JUN-1998;  
 FEATURES  
 source  
 1. 33  
 /organism="unknown"  
 BASE COUNT 9 a 7 c 7 g 10 t  
 ORIGIN

Query Match 13.2% Score 15.8; DB 6; Length 33;  
 Best Local Similarity 74.1%; Pred. No. 1e+06;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 43 CACTCCAGAGGATTCAGGGGTTCCAG 69  
 DB 28 CACTCCAGAGGATTCAGGGGTTCCAG 2  
 RESULT 48  
 S39354/c  
 LOCUS S39354 41 bp RNA linear VRL 08-MAY-1993  
 DEFINITION glycoprotein M... glycoprotein L [intergenic junction] [Pneumovirus sp.-bovine respiratory syncytial virus BRSV, strain A51908, Genomic RNA, 8 genes, 41 nt, segment 2 of 7].

ACCESSION S39354  
 VERSION S39354.1 GI:250936  
 KEYWORDS  
 SEGMENT 2 of 7  
 SOURCE Pneumovirus  
 ORGANISM Pneumovirus  
 Viruses; ssRNA negative strand viruses; Mononegavirales;  
 Paramyxoviridae; Pneumovirinae.  
 REFERENCE 1 (bases 1 to 41)  
 AUTHORS Zamora, M. and Samal, S.K.  
 TITLE Gene junction sequences of bovine respiratory syncytial virus  
 JOURNAL Virus Res. 24 (1): 115-121 (1992)  
 MEDLINE 92327836  
 PUBMED 1626423  
 REMARK Genbank staff at the National Library of Medicine created this entry [NCBI gibbsq 1083421 from the original journal article. This sequence comes from Fig. 1.

FEATURES  
 source  
 1. 41  
 /organism="Pneumovirus"  
 /strain="A51908"  
 /db\_xref="taxon:11245"  
 Join[S39353:1:22...43:1...19]  
 /partial  
 /gene="glycoprotein P"  
 BASE COUNT 10 a 9 c 5 g 17 t  
 ORIGIN

Query Match 13.2% Score 15.8; DB 14; Length 41;  
 Best Local Similarity 65.7%; Pred. No. 1e+06;  
 Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 55 ATTCAGGCTTCACGCTTCCTGAATGATCGAT 89  
 DB 41 ATACAGAGGTATAACCGGCTTAAATGATCGAT 7

RESULT 49  
 A84825/c  
 LOCUS A84825 44 bp DNA linear PAT 21-JAN-2000  
 DEFINITION Sequence 20 from Patent WO9844121.  
 ACCESSION A84825  
 VERSION A84825.1 GI:6733650  
 KEYWORDS Human adenovirus type 5.  
 SOURCE Human adenovirus type 5.  
 ORGANISM Human adenovirus type 5.  
 Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

REFERENCE 1 (bases 1 to 44)  
 AUTHORS Mehtali, M. and Legland, V.  
 TITLE MODIFIED ADENOVIRAL FIBER AND TARGET ADENOVIRUSES  
 JOURNAL Patent: WO 9844121-A 20 08-OCT-1998;  
 MEHTALI MAJID (FR); LEGRAND VALERIE (FR)  
 FEATURES  
 source  
 1. 44  
 /organism="Human adenovirus type 5"  
 /strain="ADENOVIRUS 5"  
 /isolate="OLIGONUCLEOTIDE DE SYNTHÈSE OTGE (RDNPL. G443 EN D)"  
 /db\_xref="taxon:28285"

BASE COUNT 17 a 11 c 7 g 9 t  
 ORIGIN

Query Match 13.2%; Score 15.8; DB 6; Length 44;  
 Best Local Similarity 60.5%; Pred. No. 1e+06;  
 Matches 26; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 62 GTTCCAGCGTCTCTGAAATGATGATGCTGCTTCCATAGCTG 104  
 Db 44 GTTTCAGTTTGGCTGTAAAGACAGCTTGGCTCCATATCTG 2

RESULT 50  
 AX080788/c  
 LOCUS AX080788 45 bp DNA linear PAT 27-FEB-2001  
 DEFINITION Sequence 34 from Patent WO0109327.  
 ACCESSION AX080788  
 VERSION AX080788.1 GI:13169762  
 KEYWORDS synthetic construct.  
 SOURCE synthetic construct.  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 45)  
 AUTHORS Ashkenazi, A.J., Baker, K.P., Goddard, A., Godowski, P.J., Gurney, A.D., Kijavini, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pitti, R.M., Watanabe, C.K., and Wood, W.I.  
 TITLE Method of preventing the injury or death of retinal cells and treating ocular diseases  
 JOURNAL Patent: WO 0109327-A 34 08-FEB-2001;  
 Genentech, Inc. (US)  
 FEATURES Location/Qualifiers  
 source 1..45  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="Oligonucleotide used in the isolation of DNA44167."

BASE COUNT 8 a 11 c 15 g 11 t  
 ORIGIN  
 Query Match 13.2%; Score 15.8; DB 6; Length 45;  
 Best Local Similarity 74.1%; Pred. No. 1e+06;  
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 29 CACCTCATATCCCTCCAGAGGGA 55  
 Db 28 CCCCATACTCCACCCCGAGGGA 2

RESULT 51  
 AX107698  
 LOCUS AX107698 47 bp DNA linear PAT 30-APR-2001  
 DEFINITION Sequence 517 from Patent WO0123606.  
 ACCESSION AX107698  
 VERSION AX107698.1 GI:13931183  
 KEYWORDS Streptomyces ambifaciens.  
 SOURCE Streptomyces ambifaciens.  
 ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 Actinomycetales; Streptomyceae; Streptomycetaceae; Streptomyces.  
 REFERENCE 1 (bases 1 to 47)  
 AUTHORS Grabowski, R. and Berghof, K.  
 TITLE Nucleic acid molecules for detecting bacteria and phylogenetic units of bacteria  
 JOURNAL Patent: WO 0123606-A 517 05-APR-2001;  
 Biotechon Diagnostics GmbH (DE)  
 FEATURES Location/Qualifiers  
 source 1..47  
 /organism="Streptomyces ambifaciens"  
 /db\_xref="taxon:1889"

BASE COUNT 9 a 9 c 15 g 14 t  
 ORIGIN  
 Query Match 13.2%; Score 15.8; DB 6; Length 47;  
 Best Local Similarity 65.7%; Pred. No. 1e+06;  
 Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 46 TCCAGGGGATTCAGGGGTTCCAGGCTTCCTGAAA 80

Db 6 TTCATAGCTTTTCGGTGGTCATAGCGTTAGGAAA 40

RESULT 52  
 AR005179  
 LOCUS AR005179 27 bp DNA linear PAT 04-DEC-1998  
 DEFINITION Sequence 36 from patent US 5747641.  
 ACCESSION AR005179  
 VERSION AR005179.1 GI:3966058  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 27)  
 AUTHORS Frankel, A., Pabo, C., Barsom, J.G., Fawell, S.E. and Pepinsky, R. Blake  
 TITLE Tat-derived transport polypeptide conjugates  
 JOURNAL Patent: US 5747641-A 36 05-MAY-1998;  
 FEATURES Location/Qualifiers  
 source 1..27  
 /organism="unknown"

BASE COUNT 8 a 8 c 7 g 4 t  
 ORIGIN  
 Query Match 13.0%; Score 15.6; DB 6; Length 27;  
 Best Local Similarity 81.8%; Pred. No. 1.2e+06;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GATGCCATAGTACCCCTCCTAA 24  
 Db 6 GAAGCCATGGTGACTCTCCCAA 27

RESULT 53  
 AR038389  
 LOCUS AR038389 27 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 36 from patent US 5804604.  
 ACCESSION AR038389  
 VERSION AR038389.1 GI:5957106  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 27)  
 AUTHORS Frankel, A., Pabo, C., Barsom, J.G., Fawell, S.E. and Pepinsky, R. Blake  
 TITLE Tat-derived transport polypeptides and fusion proteins  
 JOURNAL Patent: US 5804604-A 36 08-SEP-1998;  
 FEATURES Location/Qualifiers  
 source 1..27  
 /organism="unknown"

BASE COUNT 8 a 8 c 7 g 4 t  
 ORIGIN  
 Query Match 13.0%; Score 15.6; DB 6; Length 27;  
 Best Local Similarity 81.8%; Pred. No. 1.2e+06;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GATGCCATAGTACCCCTCCTAA 24  
 Db 6 GAAGCCATGGTGACTCTCCCAA 27

RESULT 54  
 AR178125  
 LOCUS AR178125 27 bp DNA linear PAT 18-DEC-2001  
 DEFINITION Sequence 36 from patent US 6316003.  
 ACCESSION AR178125  
 VERSION AR178125.1 GI:17921018  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unknown.

Query Match	13.0%	Score 15.6:	DB 6:	Length 27:
Best Local Similarity	81.8%:	Pred No. 1.2e-06:		
Matches	18:	Conservative	0:	Mismatches 4: Indels 0: Gaps 0:
QY	3	GATCCCATAGTGACCCCTCTAA	24	
DB	6	GAAGCCATGGTACTCTCCAA	27	
RESULT 57				
LOCUS	168230		37 bp	DNA
DEFINITION	Sequence 36 from patent US 5674980.			Linear
ACCESSION	168230			
VERSION	168230.1	GI:2830352		
KEYWORDS	UNKNOWN.			
ORGANISM	Unclassified			
REFERENCE	1 (bases 1 to 27)			
AUTHORS	Frankel, A., Faub, C., Barsoun, J. G., Fawell, S. E. and			
TITLE	Pepinsky, R. Blake			
JOURNAL	Fusion protein comprising tat-derived transport moiety			
FEATURES	Patent: US 5674980-A 36 01-OCT-1997;			
SOURCE	Location/Qualifiers			
	1..27			
BASE COUNT	8 a	8 c	7 g	4 t
ORIGIN	/organism='unknown'			
Query Match	13.0% <td>Score 15.6:<td>DB 6:<td>Length 27:</td></td></td>	Score 15.6: <td>DB 6:<td>Length 27:</td></td>	DB 6: <td>Length 27:</td>	Length 27:
Best Local Similarity	81.8%:	Pred No. 1.2e-06:		
Matches	18:	Conservative	0:	Mismatches 4: Indels 0: Gaps 0:
QY	3	GATCCCATAGTGACCCCTCTAA	24	
DB	6	GAAGCCATGGTACTCTCCAA	27	
RESULT 58				
LOCUS	ARI143573/c		31 bp	DNA
DEFINITION	Sequence 29 from patent US 6204371.			Linear
ACCESSION	ARI143573			
VERSION	ARI143573.1	GI:15104859		
KEYWORDS	UNKNOWN.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 31)			
AUTHORS	Levinson, D. Adam			
TITLE	Compositions and methods for the treatment and diagnosis of immune disorders			
JOURNAL	Patent: US 6204371-A 29 20-MAR-2001;			
FEATURES	Location/Qualifiers			
SOURCE	1..31			
BASE COUNT	5 a	8 c	12 g	6 t
ORIGIN	/organism='unknown'			
Query Match	13.0% <td>Score 15.6:<td>DB 6:<td>Length 31:</td></td></td>	Score 15.6: <td>DB 6:<td>Length 31:</td></td>	DB 6: <td>Length 31:</td>	Length 31:
Best Local Similarity	70.0%:	Pred No. 1.2e-06:		
Matches	21:	Conservative	0:	Mismatches 9: Indels 0: Gaps 0:
QY	42	CCATCGCAGAGGATTCAGGTTCCACGC	71	
DB	31	CCACCCAGGACGATTTCATGGTACCCGC	2	
RESULT 59				
LOCUS	ARI168942/c		31 bp	DNA
DEFINITION	Sequence 29 from patent US 6288218.			Linear







ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 48)
TITLE	Yelton,D., Glaser,S., Huse,W. and Rosok,M.Joanne. Mutant BR96 antibodies reactive with human carcinomas
JOURNAL	Patent: US 5792456-A 34 11-AUG-1998:
FEATURES	Location/Qualifiers 1..48 source
BASE COUNT	20 a 10 c 8 g 10 t
ORIGIN	/organism="unknown"
Query Match	13.0% Score 15.6; DB 6; Length 48;
Best Local Similarity	58.7%; Pred.No.1.2e+06;
Matches	27; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Oy	23 AACCCACACCTATTATCCCCACTCCAGAGGGGATTCAGGGGTCCA 68                                Db 1 AACCCAAATACATGTATACTCACTGAAGAAGTGAATCCAGAGGTACA 46 1..48 source
RESULT 68	
AX026768	
LOCUS	AX026768 48 bp DNA linear PAT 16-SEP-2000
DEFINITION	Sequence 12 from Patent WO0040712.
ACCESSION	AX026768
VERSION	AX026768.1 GI:10187907
KEYWORDS	synthetic construct.
SOURCE	synthetic construct artificial sequences.
REFERENCE	1 (bases 1 to 48) Tawfik,D. and Griffiths,A. Optical sorting method TITLE Patent: WO 0040712-A 12 13-JUL-2000; JOURNAL MEDICAL RES COUNCIL (GB); TAWFIK DAN (GB) ; GRIFFITHS ANDREW (GB)
FEATURES	Location/Qualifiers 1..48 source
BASE COUNT	15 a 14 c 9 g 10 t
ORIGIN	/organism="synthetic construct" /db_xref="taxon:32630" /note="Oligonucleotide primer"
Query Match	13.0% Score 15.6; DB 5; Length 48;
Best Local Similarity	81.8%; Pred.No.1.2e+06;
Matches	18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy	30 ACCTCATTTCCCCTCCAGC 51                        Db 13 ACCTTATTACCGCGCTCCAGA 34 1..48 source
RESULT 69	
AX026768	
LOCUS	AX026768 48 bp DNA linear PAT 01-DEC-1998
DEFINITION	Sequence 34 from patent US 5728821.
ACCESSION	AX026768
VERSION	AX026768.1 GI:3937330
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 48) Yelton,D., Glaser,S., Huse,W. and Rosok,M.Joanne. Mutant BR96 antibodies reactive with human carcinomas TITLE Patent: US 5728821-A 34 17-MAR-1998;
JOURNAL	Location/Qualifiers 1..48 source
BASE COUNT	20 a 10 c 8 g 10 t
ORIGIN	/organism="unknown"
Query Match	13.0% Score 15.6; DB 6; Length 48;
Best Local Similarity	58.7%; Pred.No.1.2e+06;
Matches	27; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Oy	23 AACCCACACCTATTATCCCCACTCCAGAGGGGATTCAGGGGTCCA 68                                Db 1 AACCCAAATACATGTATACTCACTGAAGAAGTGAATCCAGAGGTACA 46 1..48 source
RESULT 70	
AX026768	
LOCUS	AX026768 49 bp DNA linear PAT 21-JAN-2000
DEFINITION	Sequence 5 from Patent WO9902671.
ACCESSION	AX026768
VERSION	AX026768.1 GI:6731789
KEYWORDS	unidentified.
SOURCE	unidentified
ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 49) Tawfik,D. and Griffiths,A. IN VITRO SORTING METHOD TITLE Patent: WO 9902671-A 5 21-JAN-1999; JOURNAL MEDICAL RES COUNCIL (GB); TAWFIK DAN (GB)
FEATURES	Location/Qualifiers 1..49 source
BASE COUNT	15 a 14 c 10 g 10 t
ORIGIN	/organism="unidentified" /db_xref="taxon:32644"
Query Match	13.0% Score 15.6; DB 6; Length 49;
Best Local Similarity	81.8%; Pred.No.1.2e+06;
Matches	18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy	30 ACCTCATTTCCCCTCCAGC 51                        Db 13 ACCTTATTACCGCGCTCCAGA 34 1..49 source
RESULT 71	
AX076918/c	
LOCUS	AX076918 50 bp DNA linear PAT 22-FEB-2001
DEFINITION	Sequence 30 from Patent WO0105836.
ACCESSION	AX076918
VERSION	AX076918.1 GI:13121574
KEYWORDS	synthetic construct.
SOURCE	synthetic construct artificial sequences.
REFERENCE	1 (bases 1 to 50) Botstein,D., Goddard,A., Gurney,A.L., Hillan,K.J., Roy,M.A. and Wood,W.I. Polypeptidic compositions and methods for the treatment of tumors TITLE Patent: WO 0105836-A 30 25-JAN-2001;
JOURNAL	Genentech, Inc. (US)
FEATURES	Location/Qualifiers 1..50 source
BASE COUNT	8 a 16 c 11 g 15 t
ORIGIN	/organism="synthetic construct" /db_xref="taxon:32630" /note="Synthetic Oligonucleotide probe"
Query Match	13.0% Score 15.6; DB 6; Length 50;
Best Local Similarity	81.8%; Pred.No.1.3e+06;
Matches	18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Oy	86 CGATTGGCTTCCATAGCTGCTG 107                           Db 29 CCATCGGATGCCACAGCTGCTG 8 1..50 source

RESULT 72  
AX098266/c  
LOCUS AX098266 50 bp DNA linear PAT 02-APR-2001  
DEFINITION Sequence 5 from Patent WO0119987.  
ACCESSION AX098266  
VERSION AX098266.1 GI:13537572  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Fong, S., Gerritsen, M.E., Goddard, A., Gutney, A.L., Millan, K.J.,  
Williams, P.M. and Wood, W.I.  
TITLE Promotion or inhibition of angiogenesis and cardiovascularization  
JOURNAL Patent: WO 0119987-A 5 22-MAR-2001;  
Genentech, Inc. (US)  
FEATURES  
source  
Location/Qualifiers  
1..50  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Synthetic Oligonucleotide Probe"  
BASE COUNT 8 a 16 c 11 g 15 t  
ORIGIN  
Query Match 13.04; Score 15.6; DB 6; Length 50;  
Best Local Similarity 81.84; Pred. No. 1.3e+06;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 86 CGATGCGCTTCATAGTCTCTG 107  
DB 29 CCGATCCACACAGCTCTG 8  
10/20

RESULT 73  
S60243/c  
LOCUS S60243 50 bp DNA linear ROD 23-JUL-1993  
DEFINITION IGH D3 (clone 8.1) (mice, pre-B cells, blood, genomic, 50 nt).  
ACCESSION S60243  
VERSION S60243.1 GI:300004  
KEYWORDS  
SOURCE Mus sp. blood pre-B cells.  
ORGANISM Mus sp.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Rolink, A., Maasner, D., Nishikawa, S. and Melchers, F.  
TITLE Changes in frequencies of clonable pre B cells during life in  
JOURNAL different lymphoid organs of mice  
MEDLINE Blood 81 (9), 2290-2300 (1993)  
PUBMED 9324421  
REMARK 7683215  
GenBank staff at the National Library of Medicine created this  
entry [NCBI gisbq 131034] from the original journal article.  
This sequence comes from Table 2.  
FEATURES  
source  
Location/Qualifiers  
1..50  
/organism="Mus sp."  
/db\_xref="taxon:10095"  
gene partial  
/gene="IGH D3"  
BASE COUNT 11 a 8 c 14 g 17 t  
ORIGIN  
Query Match 13.04; Score 15.6; DB 10; Length 50;  
Best Local Similarity 63.24; Pred. No. 1.3e+06;  
Matches 24; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
OY 1 TCGATCCATAGTGACCTCTTACCCACACCTCATTA 38  
DB 43 TCCATAGCTAGTACCCCGGTAGCTACTACGCTAGTA 6

RESULT 74  
AX343940/c  
LOCUS AX343940 30 bp DNA linear PAT 01-FEB-2002  
DEFINITION Sequence 10 from Patent WO0200501.  
ACCESSION AX343940  
VERSION AX343940.1 GI:18491979  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Badur, R., Geiger, M., Kinze, I. and Sommer, S.  
TITLE Changing the fine chemical content in organisms by genetically  
JOURNAL modifying the shikimate pathway  
Patent: WO 0200901-A 10 03-JAN-2002;  
Sungene GmbH & Co. KGAA (DE)  
FEATURES  
source  
Location/Qualifiers  
1..30  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Primer"  
BASE COUNT 7 a 4 c 10 g 9 t  
ORIGIN  
Query Match 12.84; Score 15.4; DB 6; Length 30;  
Best Local Similarity 76.04; Pred. No. 1.4e+06;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
OY 7 CCATGACCTCTCTTACCCACAC 31  
DB 30 CCATATTAACCTCTTACCCACCC 6

RESULT 75  
AX464823  
LOCUS AX464823 37 bp DNA linear PAT 16-JUL-2002  
DEFINITION Sequence 94 from Patent WO0208401.  
ACCESSION AX464823  
VERSION AX464823.1 GI:21895524  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Mukerji, P., Das, T., Huang, Y.S., Parker-Barnes, J.M., Leonard, A.E.,  
Thurmond, J. and Pereira, S.L.  
TITLE Elongase genes and uses thereof  
JOURNAL Patent: WO 0208401-A 94 31-JAN-2002;  
Abbott Laboratories (US)  
FEATURES  
source  
Location/Qualifiers  
1..37  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Primer R0514"  
BASE COUNT 10 a 8 c 7 g 12 t  
ORIGIN  
Query Match 12.84; Score 15.4; DB 6; Length 37;  
Best Local Similarity 66.74; Pred. No. 1.4e+06;  
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
OY 51 AGCGATTACGGCTTCACCGCTCTCGAAATG 83  
DB 5 ATGGATCCATGATTCACCTCGTACATCATG 37

RESULT 76  
AR036028  
LOCUS AR036028 39 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 55 from patent US 5871974.  
ACCESSION AR036028  
VERSION AR036028.1 GI:5952696

KEYWORDS: Unknown.  
SOURCE: Unknown.  
ORGANISM: Unclassified.

REFERENCE 1 (bases 1 to 39)  
AUTHORS: Huse, W.D.  
TITLE: Surface expression libraries of heteromeric receptors  
JOURNAL: Patent: US 5871974-A 55 16-FEB-1999;  
FEATURES: Location/Qualifiers  
source 1..39  
/organism="unknown"

BASE COUNT 10 a 9 c 9 g 11 t  
ORIGIN

Query Match 12.8% Score 15.4; DB 6; Length 39;  
Best Local Similarity 66.7% Pred. No. 1.4e+06;  
Matches 22: Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 80 AATGATGATTCGCTTCATAGCTGCTGAATTG 112  
DB 5 AATACCTATTGCTACGCGAGCGCTGGATTG 37

RESULT 77  
AX006840  
LOCUS: AX006840  
DEFINITION: Sequence 6 from patent US 6180363.  
ACCESSION: AX006840  
VERSION: AX006840.1 GI:14113364  
KEYWORDS: Synthetic construct, artificial sequences.  
SOURCE: ORGANISM: Synthetic construct, artificial sequences.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS: Goller, S., Klein, D., Guenzburg, W. and Salmons, B.  
TITLE: Targeted integration into chromosomes using retroviral vectors  
JOURNAL: Patent: WO 0001835-A 14 13-JAN-2000;  
COLLER SABINE (AT); KLEIN DIETER (AT); GUENZBURG WALTER (AT); SALMONS BRIAN (DE); BAVARIAN NORDIC RES INST AS (DK)

FEATURES: Location/Qualifiers  
source 1..39  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="primer"

BASE COUNT 8 a 13 c 10 g 8 t  
ORIGIN

Query Match 12.8% Score 15.4; DB 6; Length 39;  
Best Local Similarity 66.7% Pred. No. 1.4e+06;  
Matches 22: Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 88 ATTGCTTCATAGCTGCTGAATTGCTGATTAG 120  
DB 3 ATAGCCCCCATGCGCTCGCATCGCAGCTTGG 35

RESULT 80  
AX023062  
LOCUS: AX023062  
DEFINITION: Sequence 6 from patent EP0911404.  
ACCESSION: AX023062  
VERSION: AX023062.1 GI:10046530  
KEYWORDS: unidentified, unclassified.  
SOURCE: ORGANISM: unidentified, unclassified.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS: Herck-Reichardt, D., Durst, F., Schalk, M. and Batard, Y.  
TITLE: Recoding dna sequences for expression in yeast and transformed yeasts obtained  
JOURNAL: Patent: EP 0911404-A 6 28-APR-1999;  
RHONE POULENC AGROCHIMIE (FR)

FEATURES: Location/Qualifiers  
source 1..39  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 11 a 8 c 9 g 11 t  
ORIGIN

Query Match 12.8% Score 15.4; DB 6; Length 39;  
Best Local Similarity 66.7% Pred. No. 1.4e+06;  
Matches 22: Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 68 AGCGTCTCGAAATGATGATTCGCTTCATA 100  
DB 6 AGAATTCGATTAGCGCTCGAGCTTCGAGA 38

RESULT 78  
AR161825  
LOCUS: AR161825  
DEFINITION: Sequence 27 from patent US 6258530.  
ACCESSION: AR161825  
VERSION: AR161825.1 GI:16228792  
KEYWORDS: Unknown.  
SOURCE: ORGANISM: Unknown.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS: Huse, W.D.  
TITLE: Surface expression libraries of randomized peptides  
JOURNAL: Patent: US 6258530-A 27 10-JUL-2001;  
FEATURES: Location/Qualifiers  
source 1..39  
/organism="unknown"

BASE COUNT 10 a 9 c 9 g 11 t  
ORIGIN

Query Match 12.8% Score 15.4; DB 6; Length 39;  
Best Local Similarity 66.7% Pred. No. 1.4e+06;  
Matches 22: Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 68 AGCGTCTCGAAATGATGATTCGCTTCATA 100  
DB 6 AGAATTCGATTAGCGCTCGAGCTTCGAGA 38

RESULT 78  
AR161825  
LOCUS: AR161825  
DEFINITION: Sequence 27 from patent US 6258530.  
ACCESSION: AR161825  
VERSION: AR161825.1 GI:16228792  
KEYWORDS: Unknown.  
SOURCE: ORGANISM: Unknown.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS: Huse, W.D.  
TITLE: Surface expression libraries of randomized peptides  
JOURNAL: Patent: US 6258530-A 27 10-JUL-2001;  
FEATURES: Location/Qualifiers  
source 1..39  
/organism="unknown"

BASE COUNT 10 a 9 c 9 g 11 t  
ORIGIN

Query Match 12.8% Score 15.4; DB 6; Length 39;  
Best Local Similarity 66.7% Pred. No. 1.4e+06;  
Matches 22: Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 68 AGCGTCTCGAAATGATGATTCGCTTCATA 100  
DB 6 AGAATTCGATTAGCGCTCGAGCTTCGAGA 38

KEYWORDS: Unknown.  
SOURCE: Unknown.  
ORGANISM: Unclassified.

REFERENCE 1 (bases 1 to 39)  
AUTHORS: Huse, W.D.  
TITLE: Surface expression libraries of heteromeric receptors  
JOURNAL: Patent: US 5871974-A 55 16-FEB-1999;  
FEATURES: Location/Qualifiers  
source 1..39  
/organism="unknown"

BASE COUNT 10 a 9 c 9 g 11 t  
ORIGIN

Query Match 12.8% Score 15.4; DB 6; Length 39;  
Best Local Similarity 66.7% Pred. No. 1.4e+06;  
Matches 22: Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 80 AATGATGATTCGCTTCATAGCTGCTGAATTG 112  
DB 5 AATACCTATTGCTACGCGAGCGCTGGATTG 37

RESULT 79  
AX006840  
LOCUS: AX006840  
DEFINITION: Sequence 14 from Patent WO0001835.  
ACCESSION: AX006840  
VERSION: AX006840.1 GI:9994856  
KEYWORDS: Synthetic construct, artificial sequences.  
SOURCE: ORGANISM: Synthetic construct, artificial sequences.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS: Goller, S., Klein, D., Guenzburg, W. and Salmons, B.  
TITLE: Targeted integration into chromosomes using retroviral vectors  
JOURNAL: Patent: WO 0001835-A 14 13-JAN-2000;  
COLLER SABINE (AT); KLEIN DIETER (AT); GUENZBURG WALTER (AT); SALMONS BRIAN (DE); BAVARIAN NORDIC RES INST AS (DK)

FEATURES: Location/Qualifiers  
source 1..39  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="primer"

BASE COUNT 8 a 13 c 10 g 8 t  
ORIGIN

Query Match 12.8% Score 15.4; DB 6; Length 39;  
Best Local Similarity 66.7% Pred. No. 1.4e+06;  
Matches 22: Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 88 ATTGCTTCATAGCTGCTGAATTGCTGATTAG 120  
DB 3 ATAGCCCCCATGCGCTCGCATCGCAGCTTGG 35

RESULT 80  
AX023062  
LOCUS: AX023062  
DEFINITION: Sequence 6 from Patent EP0911404.  
ACCESSION: AX023062  
VERSION: AX023062.1 GI:10046530  
KEYWORDS: unidentified, unclassified.  
SOURCE: ORGANISM: unidentified, unclassified.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS: Herck-Reichardt, D., Durst, F., Schalk, M. and Batard, Y.  
TITLE: Recoding dna sequences for expression in yeast and transformed yeasts obtained  
JOURNAL: Patent: EP 0911404-A 6 28-APR-1999;  
RHONE POULENC AGROCHIMIE (FR)

FEATURES: Location/Qualifiers  
source 1..39  
/organism="unidentified"  
/db\_xref="taxon:32644"

BASE COUNT 11 a 8 c 9 g 11 t  
ORIGIN

Query Match 12.8% Score 15.4; DB 6; Length 39;  
Best Local Similarity 66.7% Pred. No. 1.4e+06;  
Matches 22: Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 68 AGCGTCTCGAAATGATGATTCGCTTCATA 100  
DB 6 AGAATTCGATTAGCGCTCGAGCTTCGAGA 38



RESULT 86  
 ARI95274  
 LOCUS 42 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 6 from patent US 6350755.  
 ARI95274  
 VERSION 1  
 KEYWORDS  
 SOURCE /organism="unknown"  
 ORGANISM Unknown  
 REFERENCE 1 (bases 1 to 42)  
 AUTHORS Deslauriers, S. and Shaw, A.W.  
 TITLE Inhibitors of prenyl-protein transferase  
 JOURNAL Patent: US 6350755-A 6 26-FEB-2002;  
 FEATURES Location/Qualifiers  
 source 1..42  
 BASE COUNT 7 a 12 c 12 g 11 t  
 ORIGIN  
 Query Match 12.8% Score 15.4; DB 6; Length 42;  
 Best Local Similarity 66.7%; Pred. No. 1.5e+06;  
 Matches 22: Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
 Oy 44 ACTCCAGAGGATTTCAGGGTTCCAGCGTTCCT 76  
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 Db 6 AGTCTAGAGTTAACCCGTTGGTCCCGCGTTCCT 38  
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 RESULT 87  
 ARI99990  
 LOCUS 42 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 5 from patent US 6355643.  
 ARI99990  
 VERSION 1  
 KEYWORDS  
 SOURCE /organism="unknown"  
 ORGANISM Unknown  
 REFERENCE 1 (bases 1 to 42)  
 AUTHORS Luma, W.C., Sisko, J.T., Smith, A.M., Tucker, T.J., Dinsmore, C.J. and Bergman, J.M.  
 TITLE Inhibitors of prenyl-protein transferase  
 JOURNAL Patent: US 6355643-A 5 12-MAR-2002;  
 FEATURES Location/Qualifiers  
 source 1..42  
 BASE COUNT 7 a 12 c 12 g 11 t  
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 Query Match 12.8% Score 15.4; DB 6; Length 42;  
 Best Local Similarity 66.7%; Pred. No. 1.5e+06;  
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 Oy 44 ACTCCAGAGGATTTCAGGGTTCCAGCGTTCCT 76  
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 Db 6 AGTCTAGAGTTAACCCGTTGGTCCCGCGTTCCT 38  
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 RESULT 88  
 ARI201343  
 LOCUS 42 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 5 from patent US 6358956.  
 ARI201343  
 VERSION 1  
 KEYWORDS  
 SOURCE /organism="unknown"  
 ORGANISM Unknown  
 REFERENCE 1 (bases 1 to 42)  
 AUTHORS Hartman, G.D., Luma, W.C. Jr., Sisko, J.T., Smith, A.M., Tucker, T.J.

anif Stokker, G.E.  
 TITLE Inhibitors of prenyl-protein transferase  
 JOURNAL Patent: US 6358956-A 5 19-MAR-2002;  
 FEATURES Location/Qualifiers  
 source 1..42  
 BASE COUNT 7 a 12 c 12 g 11 t  
 ORIGIN /organism="unknown"  
 Query Match 12.8% Score 15.4; DB 6; Length 42;  
 Best Local Similarity 66.7%; Pred. No. 1.5e+06;  
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 Oy 44 VTCCAGAGGATTTCAGGGTTCCAGCGTTCCT 76  
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 Db 6 AGTCTAGAGTTAACCCGTTGGTCCCGCGTTCCT 38  
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 RESULT 89  
 ARI201362  
 LOCUS 42 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 6 from patent US 6358985.  
 ARI201362  
 VERSION 1  
 KEYWORDS  
 SOURCE /organism="unknown"  
 ORGANISM Unknown  
 REFERENCE 1 (bases 1 to 42)  
 AUTHORS Anthony, N.J., Bell, I.M., Beshore, D.C., Ciccarone, T.M., de Solms, S., Jane, J., Dinsmore, C.J. and Stokker, G.E.  
 TITLE Inhibitors of prenyl-protein transferase  
 JOURNAL Patent: US 6358985-A 6 19-MAR-2002;  
 FEATURES Location/Qualifiers  
 source 1..42  
 BASE COUNT 7 a 12 c 12 g 11 t  
 ORIGIN  
 Query Match 12.8% Score 15.4; DB 6; Length 42;  
 Best Local Similarity 66.7%; Pred. No. 1.5e+06;  
 Matches 22: Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
 Oy 44 ACTCCAGAGGATTTCAGGGTTCCAGCGTTCCT 76  
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 RESULT 90  
 ARI205929  
 LOCUS 42 bp DNA linear PAT 31-JAN-2002  
 DEFINITION Human B-cell translocation genes-2 and 3.  
 ARI205929  
 VERSION 1  
 KEYWORDS  
 SOURCE /organism="unknown"  
 ORGANISM Unknown  
 REFERENCE 1 (bases 1 to 42)  
 AUTHORS Knirsch, C.A., Chopra, A. and Rosen, C.A.  
 TITLE Human B-cell translocation genes-2 and 3  
 JOURNAL Patent: JP 2001501464-A 6 06-FEB-2001;  
 COMMENT HUMAN GENOME SCIENCES INC  
 OS Unidentified  
 PN JP 2001501464-A/6  
 PD 06-FEB-2001  
 PF 18-SEP-1996 JP 1998514608  
 PH  
 PI CHARLES A. KUNSCH, ARVIND CHOPRA, CRAIG A. ROSEN  
 PC C07H21/04, C12P21/02, C12P21/08, C07K16/00, C07K14/475, A61K38/00  
 CC Strandedness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers

FT source 1.42  
 /organism="Unidentified"  
 Location/Qualifiers  
 1.42  
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 /db\_xref="taxon:32644"  
 9 a 11 c 15 g 7 t

BASE COUNT  
 9 a 11 c 15 g 7 t

ORIGIN

Query Match 12.8% Score 15.4; DB 6; Length 42;  
 Best Local Similarity 61.0%; Pred. No. 1.5e+06;  
 Matches 25; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 58 CAGGGTTCACGGTCTCTCGAATGATGATGCTTCCA 98  
 ||||| 111 1 1 1 1111 11  
 DB 1 CAGTGATCCACGCCGACGATGATGCTCAGTTGCCACGA 41

RESULT 91  
 AGRN1/c

LOCUS  
 DEFINITION Anopheles gambiae 28S rDNA fragment containing 5' end of insertion  
 sequence.  
 ACCESSION X15305  
 VERSION X15305.1 GI:5601  
 KEYWORDS 28S ribosomal RNA; insertion sequence; ribosomal DNA; ribosomal RNA.  
 SOURCE African malaria mosquito.  
 ORGANISM Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.

REFERENCE  
 Paskewitz S.M. and Collins F.H.  
 TITLE Site specific ribosomal DNA insertion elements in Anopheles gambiae and A. tritaeniorhynchus: nucleotide sequence of a gene element boundaries  
 JOURNAL Nucleic Acids Res. 17 (20): 8125-8133 (1989)  
 MEDLINE 90045938  
 PUBMED 2554252

REFERENCE  
 2 (bases 1 to 43)  
 Paskewitz S.M.  
 AUTHORS Direct Submission  
 TITLE Submitted (12-MAY-1989) Paskewitz S.M., Centres for Disease Control, Malaria Branch F12, CID/CDC, Atlanta Georgia 30333, U S A  
 JOURNAL Location/Qualifiers

FEATURES  
 source 1.43  
 /organism="Anopheles gambiae"  
 /strain="G3"  
 /db\_xref="taxon:7165"  
 /chromosome="chromosome X"  
 /clone="lambda Agr7BH4.5, 5' end"  
 /clone\_lib="lambda EMBL3"  
 /dev\_stage="adult"  
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 /product="28S ribosomal RNA"  
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 /insertion\_seq="insertion sequence 5' end"

BASE COUNT 10 a 11 c 12 g 10 t

ORIGIN

Query Match 12.8% Score 15.4; DB 3; Length 43;  
 Best Local Similarity 61.0%; Pred. No. 1.5e+06;  
 Matches 25; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 30 ACCGATATATCCCTACCTCCAGAGGATTCAGGGGTTCCAGC 70  
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 DB 42 ACCGATATATCCCTACCTACACAGGATTCAGGGGTTGTCG 2

RESULT 92  
 AX175335

LOCUS  
 DEFINITION Sequence 24 from Patent WO0204523.  
 ACCESSION AX375335  
 VERSION AX375335.1 GI:19159959  
 KEYWORDS synthetic construct;  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE  
 1  
 Koide, S.  
 AUTHORS Artificial antibody polypeptides  
 TITLE Patent: WO 0204523-A 24 17-JAN-2002;  
 JOURNAL Research Corporation Technologies, Inc (US); Koide, Shohei (US)  
 LOCATION/Qualifiers  
 1.44  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="Oligonucleotide gene3P."

BASE COUNT 10 a 12 c 11 g 11 t

ORIGIN

Query Match 12.8% Score 15.4; DB 6; Length 44;  
 Best Local Similarity 66.7%; Pred. No. 1.5e+06;  
 Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 52 GCGATTCAGGGGTTCCAGCGCTTCCTCGAATATCA 84  
 ||||| 11 11 11 1111 1111 11 11  
 DB 2 GCGATTCAGCGGTCCTTCCTTCGTAATATCA 34

RESULT 93  
 BD006278

LOCUS  
 DEFINITION Artificial antibody polypeptides.  
 ACCESSION BD006278  
 VERSION BD006278.1 GI:18634649  
 KEYWORDS JP 2001500531-A/12.  
 SOURCE unidentified  
 ORGANISM unclassified  
 REFERENCE 1 (bases 1 to 44)  
 Koide, S.  
 AUTHORS Artificial antibody polypeptides  
 TITLE Patent: JP 2001500531-A 12 16-JAN-2001;  
 JOURNAL RESEARCH CORPORATION TECHNOLOGIES INC  
 COMMENT OS Unidentified  
 PN JP 2001500531-A/12  
 PD 16-JAN-2001  
 PF 12-JUN-1998 JP 1999503195  
 PR 12-JUN-1997 US 60/049410  
 P1 SHOEI KOIDE  
 PC G12N15/12.C07K14/78.G12N15/70.G12N1/21  
 CC Strandedness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers  
 FT source 1.44  
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 source 1.44  
 Location/Qualifiers  
 1.44  
 /organism="unidentified"  
 /db\_xref="taxon:32644"

BASE COUNT 10 a 12 c 11 g 11 t

ORIGIN

Query Match 12.8% Score 15.4; DB 6; Length 44;  
 Best Local Similarity 66.7%; Pred. No. 1.5e+06;  
 Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 52 GCGATTCAGGGGTTCCAGCGCTTCCTCGAATATCA 84  
 ||||| 11 11 11 1111 1111 11 11  
 DB 2 GCGATTCAGCGGTCCTTCCTTCGTAATATCA 34

RESULT 94  
LOCUS AR125804/c 50 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 146 from patent US 6177557.  
ACCESSION AR125804  
VERSION AR125804.1 GI:14111866  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Janjic,N., Gold,L. and Tasset,D.  
TITLE High affinity ligands of basic fibroblast growth factor and thrombin  
JOURNAL Patent: US 6177557-A 146 23-JAN-2001;  
FEATURES Location/Qualifiers  
source 1..50  
BASE COUNT 12 a 9 c 19 g 10 t  
ORIGIN  
Query Match 12.84; Score 15.4; DB 6; Length 50;  
Best Local Similarity 94.14; Pred. No. 1.5e+06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 16 CCCTCCTTAACCCACACC 32  
Db 47 CCCTCCTTAACCCACACC 31  
RESULT 95  
LOCUS AR125842/c 50 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 184 from patent US 6177557.  
ACCESSION AR125842  
VERSION AR125842.1 GI:14111904.  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Janjic,N., Gold,L. and Tasset,D.  
TITLE High affinity ligands of basic fibroblast growth factor and thrombin  
JOURNAL Patent: US 6177557-A 184 23-JAN-2001;  
FEATURES Location/Qualifiers  
source 1..50  
BASE COUNT 12 a 9 c 19 g 10 t  
ORIGIN  
Query Match 12.84; Score 15.4; DB 6; Length 50;  
Best Local Similarity 94.14; Pred. No. 1.5e+06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 16 CCCTCCTTAACCCACACC 32  
Db 47 CCCTCCTTAACCCACACC 31  
RESULT 96  
LOCUS I47216/c 50 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 146 from patent US 5639868.  
ACCESSION I47216  
VERSION I47216.1 GI:24711181  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Janjic,N. and Gold,L.  
TITLE High-affinity RNA ligands for basic fibroblast growth factor

JOURNAL Patent: US 5639868-A 146 17-JUN-1997;  
FEATURES Location/Qualifiers  
source 1..50  
BASE COUNT 12 a 9 c 19 g 10 t  
ORIGIN  
Query Match 12.84; Score 15.4; DB 6; Length 50;  
Best Local Similarity 94.14; Pred. No. 1.5e+06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 16 CCCTCCTTAACCCACACC 32  
Db 47 CCCTCCTTAACCCACACC 31  
RESULT 97  
LOCUS I47254/c 50 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 184 from patent US 5639868.  
ACCESSION I47254  
VERSION I47254.1 GI:2471219  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Janjic,N. and Gold,L.  
TITLE High-affinity RNA ligands for basic fibroblast growth factor  
JOURNAL Patent: US 5639868-A 184 17-JUN-1997;  
FEATURES Location/Qualifiers  
source 1..50  
BASE COUNT 12 a 9 c 19 g 10 t  
ORIGIN  
Query Match 12.84; Score 15.4; DB 6; Length 50;  
Best Local Similarity 94.14; Pred. No. 1.5e+06;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 16 CCCTCCTTAACCCACACC 32  
Db 47 CCCTCCTTAACCCACACC 31  
RESULT 98  
LOCUS AX487275 20 bp DNA linear PAT 16-AUG-2002  
DEFINITION Sequence 4575 from Patent WO02053728.  
ACCESSION AX487275  
VERSION AX487275.1 GI:22321423  
KEYWORDS  
SOURCE Candida albicans.  
ORGANISM Candida albicans.  
REFERENCE 1  
AUTHORS Kemer,T., Jiang,B., Boone,C., Bussey,K. and Ohlsen,K.L.  
TITLE Gene disruption methodologies for drug target discovery  
JOURNAL Patent: WO 02053728-A 4575 11-JUL-2002;  
FEATURES Location/Qualifiers  
source 1..20  
BASE COUNT 3 a 10 c 1 g 6 t  
ORIGIN  
Query Match 12.74; Score 15.2; DB 6; Length 20;  
Best Local Similarity 85.04; Pred. No. 1.5e+06;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 27 CACACCTCATTTATCCCACT 46





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 21:13:50 : Search time 1368 Seconds  
(without alignments)  
1420.657 Million cell updates/sec

Title: US-09-676-436-3\_COPY\_3264\_3383

Perfect score: 120

Sequence: 1 tcatgcatagtcacccctc.....gcctgcatgacgttag 120

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Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102772

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

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3: en\_estin.\*  
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5: en\_estov.\*  
6: en\_estpl.\*  
7: en\_estro.\*  
8: en\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: en\_estfun.\*  
16: en\_estom.\*  
17: gb\_gss.\*  
18: en\_gss\_hum.\*  
19: en\_gss\_inv.\*  
20: en\_gss\_pln.\*  
21: en\_gss\_vrt.\*  
22: en\_gss\_fun.\*  
23: en\_gss\_mam.\*  
24: en\_gss\_mus.\*  
25: en\_gss\_Other.\*  
26: en\_gss\_POD.\*  
27: en\_gss\_FOD.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	19.6	16.3	46	17	BH621582
2	18.4	15.3	46	9	AT025674
3	18	15.0	50	9	AT03646
4	17.2	14.3	49	9	AT136193
5	17.2	14.3	50	9	AT104247
6	17.2	14.3	50	17	AL761984

AZ796134	240052101	43	17	AZ796334	14.2
AU103929	AU103929	50	9	AU103929	17
AZ960044	240227423	45	17	AZ960044	14.0
AZ450654	140366901	41	17	AZ450654	13.8
BI914625	603179586	33	13	BI914625	13.7
AZ769247	140566910	33	13	AZ769247	16.4
BI761448	603044269	35	13	BI761448	13.7
AZ853008	240155817	42	17	AZ853008	13.7
A1492250	159403	43	9	A1492250	16.4
AZ500971	140339811	36	17	AZ500971	13.5
AT198940	qf66f09.x	40	9	AT198940	16.2
AZ767497	140566008	45	17	AZ767497	13.5
AZ768968	140569909	47	17	AZ768968	16.2
A1928097	wpl1a11.x	49	9	A1928097	16.2
BH740835	KG04938-5	39	17	BH740835	13.3
AL486316	T. brucei	37	17	TA2944100	16
T61673	y887904.s1	48	14	T61673	16
AZ621174	140454008	50	17	AZ621174	13.3
AZ806715	240068019	30	17	AZ806715	13.3
AZ626127	140466007	38	17	AZ626127	15.8
AZ782425	240022314	45	17	AZ782425	13.2
AZ514366	140361002	37	17	AZ514366	13.0
AZ591306	14040117	50	9	AZ591306	13.0
AU103234	AU103234	50	9	AU103234	13.0
AZ597958	140412323	50	17	AZ597958	13.0
AZ776846	240010A20	34	17	AZ776846	12.8
AZ450959	140232022	35	17	AZ450959	12.8
AZ526803	240010020	43	17	AZ526803	12.4
A1927385	fl35112	43	17	A1927385	12.8
A1927385	fl35112	49	9	A1927385	12.8
A1927385	fl35112	49	9	A1927385	12.8
AU105911	AU105911	50	9	AU105911	12.8
AK507256	EST00684	50	10	AK507256	12.8
AK507292	EST00720	50	10	AK507292	12.8
AZ456166	140258820	50	17	AZ456166	12.8
AA904249	oe74602.s	43	9	AA904249	12.7
AA948203	oe99409.s	43	9	AA948203	12.7
AZ403273	140171G12	45	17	AZ403273	12.7
AL758605	Alcblidops	45	17	AL758605	12.7
AA826579	oe66910.s	46	9	AA826579	12.7
AK059631	HuHt.bsst	47	10	AK059631	12.7
AL656975	AL656975	48	9	AL656975	12.7
AA976736	Qg6f10.s	49	9	AA976736	12.7
AU106947	AU106947	50	9	AU106947	12.7
AU107595	AU107595	50	9	AU107595	12.7
AU107687	AU107687	50	9	AU107687	12.7
AZ307590	140009N10	50	17	AZ307590	12.7
AA908637	Qg6f07.s	55	15	AA908637	12.5
AZ636460	140495M14	33	17	AZ636460	12.5
AZ380286	140136E12	34	17	AZ380286	12.5
AZ659063	140536M10	36	17	AZ659063	12.5
AZ309443	140013011	42	17	AZ309443	12.5
A1937592	wp81d11.x	46	9	A1937592	12.5
AZ579592	140367002	47	17	AZ579592	12.5
AZ768567	140568D05	47	17	AZ768567	12.5
BH49286	SALK_0694	63	13	BH49286	12.5
AU102397	AU102397	50	9	AU102397	12.5
AU102413	AU102413	50	9	AU102413	12.5
AU165901	AU165901	50	9	AU165901	12.5
AZ381606	246270622	30	17	AZ381606	12.3
AZ637132	140188A13	30	17	AZ637132	12.3
AZ637132	140188A13	40	9	AZ637132	12.3
A1356755	Qg22f02.s	43	9	A1356755	12.3
A1356755	Qg22f02.s	45	9	A1356755	12.3
BH890364	1526.1.13	48	17	BH890364	12.3
AZ442808	140237N08	48	17	AZ442808	12.3
AZ623464	140461F15	48	17	AZ623464	12.3
AA928990	Qg27401.15	49	9	AA928990	12.3
A1185244	qg11e04.s	49	9	A1185244	12.3
AU104948	AU104948	50	9	AU104948	12.3
AU106265	AU106265	50	9	AU106265	12.3
AU106343	AU106343	50	9	AU106343	12.3

C 80	14.6	12.2	37	17	AL771100 Arabidops	153	14	11.7	49	9	AA907869	AA907869 OK79612.s
C 81	14.6	12.2	38	17	A2459577 IM0264319	C 154	14	11.7	49	9	AA907869	AA907869 OK79612.s
C 82	14.6	12.2	39	14	N75693 Y52801.11	C 155	14	11.7	49	9	AT245493	AT245493 QK30801.x
C 83	14.6	12.2	39	17	N75693 Y52801.11	C 156	14	11.7	49	10	AA476027	AA476027 VHZ6C07.f
C 84	14.6	12.2	43	9	AI351416 qg37601.x	C 157	14	11.7	49	10	AA476027	AA476027 VHZ6C07.f
C 85	14.6	12.2	45	17	A2428033 IM0210617	C 158	14	11.7	49	9	AZ768953	AZ768953 IM0569M11
C 86	14.6	12.2	46	17	A2428033 IM0210617	C 159	14	11.7	50	9	AL627930	AL627930 AL627930
C 87	14.6	12.2	45	17	A2581263 IM0369N16	C 160	14	11.7	50	9	AU102456	AU102456 AU102456
C 88	14.6	12.2	49	14	C21077 HUNG0000259	C 161	14	11.7	50	9	AU102523	AU102523 AU102523
C 89	14.6	12.2	50	9	AU102946 AU102946	C 162	14	11.7	50	9	AU102953	AU102953 AU102953
C 90	14.6	12.2	50	9	AU108029 AU108029	C 163	14	11.7	50	9	AU103938	AU103938 AU103938
C 91	14.6	12.2	50	17	A2416047 IM0191E11	C 164	14	11.7	50	9	AU104029	AU104029 AU104029
C 92	14.4	12.0	34	9	AA868967 a55904.s	C 165	14	11.7	50	9	AU104251	AU104251 AU104251
C 93	14.4	12.0	34	9	AA868967 a55904.s	C 166	14	11.7	50	9	AU106898	AU106898 AU106898
C 94	14.4	12.0	38	9	AA996016 q526d10.s	C 167	14	11.7	50	9	AU106898	AU106898 AU106898
C 95	14.4	12.0	38	17	A2424085 IM0203805	C 168	14	11.7	50	9	AU106898	AU106898 AU106898
C 96	14.4	12.0	39	17	A2424085 IM0203805	C 169	14	11.7	50	9	AU106898	AU106898 AU106898
C 97	14.4	12.0	40	9	AA973240 OT30N05.s	C 170	14	11.7	50	9	AU107601	AU107601 AU107601
C 98	14.4	12.0	40	17	BH797868 IM008096A0	C 171	14	11.7	50	9	AU107601	AU107601 AU107601
C 99	14.4	12.0	41	17	A2423755 IM0203C23	C 172	14	11.7	50	9	AU107684	AU107684 AU107684
C 100	14.4	12.0	43	2	HS4007841	C 173	13.8	11.5	26	17	BH789444	BH789444 SALK_0294
C 101	14.4	12.0	43	9	AA011545	C 174	13.8	11.5	26	17	A2345602	A2345602 IM0080A21
C 102	14.4	12.0	43	9	AA011545	C 175	13.8	11.5	29	17	A2794355	A2794355 IM0568F17
C 103	14.4	12.0	43	9	AA011545	C 176	13.8	11.5	29	17	A2794355	A2794355 IM0568F17
C 104	14.4	12.0	43	9	AA011545	C 177	13.8	11.5	33	17	A2335637	A2335637 IM0065K16
C 105	14.4	12.0	45	10	B2536392 IM0106293	C 178	13.8	11.5	33	17	A2844379	A2844379 IM0143H23
C 106	14.4	12.0	45	9	AT250043 q448f02.x	C 179	13.8	11.5	34	17	A2625604	A2625604 IM0465D16
C 107	14.4	12.0	46	13	AI094098 q433602.s	C 180	13.8	11.5	34	17	AT759611	AT759611 Arabidops
C 108	14.4	12.0	46	13	B252353 602953082	C 181	13.8	11.5	34	17	A2784558	A2784558 IM0027G15
C 109	14.4	12.0	46	17	A2828414 IM0105E23	C 182	13.8	11.5	37	17	A2989635	A2989635 IM0273K06
C 110	14.4	12.0	47	14	D18780 MUGS000496	C 183	13.8	11.5	38	17	A2506007	A2506007 IM0346P19
C 111	14.4	12.0	47	17	A2843553 IM0142A03	C 184	13.8	11.5	38	17	BH129371	BH129371 G-558.f
C 112	14.4	12.0	48	17	A2317194 IM0033512	C 185	13.8	11.5	40	9	AA878861	AA878861 Q84f09.s
C 113	14.4	12.0	50	9	AU105376 AU105376	C 186	13.8	11.5	40	9	AA878861	AA878861 Q84f09.s
C 114	14.4	12.0	50	9	AU106349 AU106349	C 187	13.8	11.5	42	17	BH641736	BH641736 IM008049F1
C 115	14.2	11.8	32	14	AU107641 AU107641	C 188	13.8	11.5	42	17	A2467316	A2467316 IM0278R08
C 116	14.2	11.8	32	14	D19573 MUGS000978	C 189	13.8	11.5	43	9	A2808588	A2808588 IM0072M12
C 117	14.2	11.8	33	14	D38731 MUG2510.x	C 190	13.8	11.5	43	9	A2808588	A2808588 IM0072M12
C 118	14.2	11.8	33	17	A464636	C 191	13.8	11.5	43	9	A2808588	A2808588 IM0072M12
C 119	14.2	11.8	39	17	A2762490	C 192	13.8	11.5	44	9	AL630890	AL630890 IM030890
C 120	14.2	11.8	40	17	A2434447	C 193	13.8	11.5	44	17	TA121E040	TA121E040 IM0569G21
C 121	14.2	11.8	40	17	A2793475	C 194	13.8	11.5	44	17	TA121E040	TA121E040 IM0569G21
C 122	14.2	11.8	41	10	AV833059	C 195	13.8	11.5	45	17	A2755586	A2755586 IM0129G03
C 123	14.2	11.8	41	17	BH889237	C 196	13.8	11.5	45	17	A2755586	A2755586 IM0129G03
C 124	14.2	11.8	43	17	BH889237	C 197	13.8	11.5	46	9	A1626090	A1626090 a187h08.x
C 125	14.2	11.8	45	17	A2443427	C 198	13.8	11.5	46	9	A1626090	A1626090 a187h08.x
C 126	14.2	11.8	45	17	A2512933	C 199	13.8	11.5	46	17	BH848309	BH848309 SALK_0677
C 127	14.2	11.8	45	17	BH808539	C 200	13.8	11.5	47	17	A2420561	A2420561 IM0198021
C 128	14.2	11.8	46	13	B1755563							
C 129	14.2	11.8	48	17	A2507309							
C 130	14.2	11.8	48	17	A2646970							
C 131	14.2	11.8	50	9	AU103596							
C 132	14.2	11.8	50	9	AU103597							
C 133	14.2	11.8	50	9	AU108006							
C 134	14.2	11.8	50	9	AU108006							
C 135	14.2	11.8	50	9	AU108006							
C 136	14.2	11.8	50	9	AU108006							
C 137	14.2	11.8	50	9	AU108006							
C 138	14.2	11.8	50	9	AU108006							
C 139	14.2	11.8	50	9	AU108006							
C 140	14.2	11.8	50	9	AU108006							
C 141	14.2	11.8	50	9	AU108006							
C 142	14.2	11.8	50	9	AU108006							
C 143	14.2	11.8	50	9	AU108006							
C 144	14.2	11.8	50	9	AU108006							
C 145	14.2	11.8	50	9	AU108006							
C 146	14.2	11.8	50	9	AU108006							
C 147	14.2	11.8	50	9	AU108006							
C 148	14.2	11.8	50	9	AU108006							
C 149	14.2	11.8	50	9	AU108006							
C 150	14.2	11.8	50	9	AU108006							
C 151	14.2	11.8	50	9	AU108006							
C 152	14.2	11.8	50	9	AU108006							

## ALIGNMENTS

RESULT 1	BH621582	1007114E09.1EL_x1 1007	46 bp	DNA	linear	GSS 30-JAN-2002
LOCUS	BH621582	1007114E09.1EL_x1 1007	46 bp	DNA	linear	GSS 30-JAN-2002
DEFINITION	BH621582	1007114E09.1EL_x1 1007	46 bp	DNA	linear	GSS 30-JAN-2002
ACCESSION	BH621582	1007114E09.1EL_x1 1007	46 bp	DNA	linear	GSS 30-JAN-2002
VERSION	BH621582.1	GI:18434812				
KEYWORDS	GSS.					
SOURCE	Zea mays.					
ORGANISM	Zea mays.					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC					
TITLE	clade; Panicoidae; Andropogoneae; Zea.					
JOURNAL	1 (bases 1 to 46)					
COMMENT	Walbot V.					
	Maize genomic sequences found using engineered RescueMu transposon					
	Unpublished (2001)					
	Contact: Walbot V					
	Department of Biological Sciences					
	Stanford University					







Best Local Similarity 80.0%; Pred. No. 2.1e+05;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GATGCCATGACCTCCCTACCC 27  
DB 11 GATGCCATGACCTCCCTACCC 35

RESULT 9  
AZ960044/c  
LOCUS  
DEFINITION  
2M0227M23R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0227M23 R, DNA sequence.  
ACCESSION  
AZ960044  
VERSION  
GI:1381271  
KEYWORDS  
GSS.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
and Wright, D., Weiss, R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0227 row: M column: 23  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 46.

## FEATURES

Source  
1. 46  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0227M23"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (G114732114) (p1AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT  
ORIGIN  
9 a 1 c 23 g 13 t

Query Match 14.0%; Score 16.8; DB 17; Length 46;

Best Local Similarity 66.7%; Pred. No. 2.3e+05;  
Matches 24; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 16 CCCTCCTAACCCACCTCATTTATCCCTCCAGCA 51  
DB 46 CCCTCCTAACCCACCTCATTTATCCCTCCAGCA 11

RESULT 10  
AZ460654/c  
LOCUS  
DEFINITION  
1M0266P01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0266P01 F, DNA sequence.  
ACCESSION  
AZ460654  
VERSION  
GI:10618779  
KEYWORDS  
GSS.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
and Wright, D., Weiss, R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0266 row: P column: 01  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 41.

FEATURES  
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/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0266P01"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (G114732114) (p1AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT  
ORIGIN  
5 a 4 c 21 g 11 t

Query Match 13.8%; Score 16.6; DB 17; Length 41;





ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 35)  
 AUTHORS NIH-MGC <http://mcc.ncbi.nlm.nih.gov/>  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM11460 row: j column: 17  
 High quality sequence stop: 35.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone\_image="5184496"  
 /clone\_lib="NIH\_MGC\_116"  
 /lab\_host="DH10B"  
 /note="organ: pooled colon, kidney, stomach; Vector:  
 pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA  
 source anonymous pool of 3 colons, age 26 yo male, 49 yo  
 female, 71 yo male kidney, and pool of 2  
 stomachs, 62 yo male and 70 yo female. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.4 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics Tracking code  
 023. Note: this is a NIH\_MGC Library."

## FEATURES

source

BASE COUNT 6 a 9 c 14 g 6 t  
 ORIGIN  
 Query Match 13.7%; Score 16.4; DB 13; Length 35;  
 Best Local Similarity 94.4%; Pred. No. 2.7e-05;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 61 GGGTCCAGCGTTCCTGA 78  
 ||||| ||||| ||||| ||||| |||||  
 Db 16 GGGTACCAGCGTTCCTGA 33

RESULT 14  
 A2853008/c  
 LOCUS 2M0155K17R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
 DEFINITION clone UUGC2M0155K17 R, DNA sequence.  
 ACCESSION A2853008  
 VERSION A2853008.1 GI:11040692  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 42)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.  
 and Wright, D. Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0155 row: k column: 17  
 Seq primer: CACACAGGAACACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 42.  
 Location/Qualifiers  
 1..42  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone\_image="UUGC2M0155K17"  
 /clone\_lib="Mouse 10kb plasmid UUGCLM library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /note="Vector: pMD22nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD22 (g11473211419b1AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## BASE COUNT

7 a 3 c 24 g 8 t

Query Match 13.7%; Score 16.4; DB 17; Length 42;  
 Best Local Similarity 61.9%; Pred. No. 3e+05;  
 Matches 26; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
 Oy 16 CCTCTTAACCCACACCTCTATTATCCCACTCCAGAGCGATT 57  
 ||| || |||| |||| || |||| |||| |||| ||||  
 Db 42 CCCACCCACCCACACCAACCTCCCTTTCCACCGCGATT 1

RESULT 15  
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 LOCUS A1492250 43 bp mRNA linear EST 30-MAR-1999  
 DEFINITION t159403.x1 NCI-CCAP Brn23 Homo sapiens cDNA clone IMAGE:2103532 3'  
 similar to TR:Q39866 Q39866 HYDROXYPROLINE-RICH GLYCOPROTEIN  
 ; Consensus MER22.t1 MSRI repetitive element .. mRNA sequence.  
 ACCESSION A1492250  
 VERSION A1492250.1 GI:4393253  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 43)  
 AUTHORS NCI/NINDS-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>  
 TITLE National Cancer Institute / National Institute of Neurological  
 Disorders and Stroke, Brain Tumor Genome Anatomy Project  
 (CCAP/BRGAP), Tumor Gene Index  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
 Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 973 Std Error: 0.00  
Seq primer: -400p from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers

## FEATURES

Source

1 43  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:210332"  
/clone\_lib="NCI CGAP Brn23"  
/tissue\_type="glioblastoma (pooled)"  
/lab\_host="DH10B"

/note="Organ: brain; Vector: p773D-Pac (Pharmacia) with a  
modified polylinker; Site: 1; Not 1; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not 1 - oligo(dT) primer [5'  
TGTACCAATCTGAAGTGGAGCGCCCATCTTTTITTTTITTTTITTTT  
7 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not 1 and cloned into  
the Not 1 and Eco RI sites of the modified p773 vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT

9 a 24 c 0 g 10 t

ORIGIN

Query Match 13.7% Score 16.4; DB 9; Length 43;  
Best Local Similarity 67.6% Pred. No. 3e+05;  
Matches 23; Conservative 0; Mismatches 11; Indels 0; Gaps 0.

Oy 16 CCTCTTACCCACACCTCATATTCCTCCACTCCA 49  
||| || ||||| ||||| | | | | | | | |  
Db 1 CCCCCAACCCCTCTCTCTCTCTCTCTCTCTCTCA 34

RESULT 16

A198940

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

A198940 36 bp DNA linear GSS 05-OCT-2000  
A198940.1 Mouse 10kb plasmid UUCIM library Mus musculus genomic  
A198940.1 R. DNA sequence.

A198940.1 GI:10682287  
GSS  
Mus musculus

Human  
Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 36)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.,  
and Wright, D., Welts, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Welts  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0339 Row: B Column: 11  
Seq primer: CACACGAGAACGCTATACC  
Class: plasmid ends  
High quality sequence stop: 36.  
Location/Qualifiers

FEATURES

Source

Source

1 36  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="UUCIM033981"  
/clone\_lib="Mouse 10kb plasmid UUCIM library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, P-"  
/note="Vector: pMD20v; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD20 (g14732141gblAF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT

11 a 5 c 10 g 10 t

ORIGIN

Query Match 13.5% Score 16.2; DB 17; Length 36;  
Best Local Similarity 72.4% Pred. No. 3.2e+05;  
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0.

Oy 36 TTATCCCTCCATCCAGAGGATTCAGGGGT 64  
||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 29 TTGTACCCCTCCATCCAGGATTCAGGGGT 1

RESULT 17

A198940

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

A198940 40 bp mRNA linear EST 27-JAN-1999  
A198940.1 Soares, Testis, NHT Homo sapiens cDNA clone IMAGE.1755017  
Y. Similar to SW:EXTN.T0BAC.P1393; EXTENSIN PRECURSOR; contains  
element MSRI repetitive element; mRNA sequence.

A198940.1 GI:3751546  
EST  
Human

Homo sapiens  
Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 40)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps@mail.nih.gov  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 620 Std Error: 0.00  
Seq primer: -400p from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers



hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones IDs J32912-J325831, J471368-J472903 and J492104-J493255). Subtraction by Bento Soares and M.

RESULT 21	19 bp DNA linear
BH740835	KG04938: <i>Spiraea Drosophila melanogaster</i> PISUPOR-P1 P element
BH740835	insertion lines <i>Drosophila melanogaster</i> genomic sequence recovered
DEFINITION	from 5' end of P element. DNA sequence.
ACCESSION	BH740835
VERSION	BH740835.1
KEYWORDS	GI:18861338
	GSS.

ORGANISM  
*Drosophila melanogaster*  
Karyotype: Metazoa: Arthropoda: Hexapoda: Insecta: Pterygota:  
Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:  
1. Phlebotominae: 2. Phlebotomidae: *Drosophila*  
Lewis, R. Hosking, R., Liao, G., Worden, N., Tseng, G., He, Y., Karpen  
G., Bellic, H., Rubin, G. and Spradling, A.  
AUTHORS  
The Berkeley Drosophila Genome Project Gene Disruption Project  
Unpublished (2001)  
TITLE  
JOURNAL

**FEATURES**

source  
locus 39  
organism="Drosophila melanogaster"  
dbxref="taxon:7227"  
clone.lib="Drosophila melanogaster PISUPOR-pJ P element insertion lines"  
note="Inverse PCR was performed on Drosophila

```

metanogaster strains each of which contains one or more
P[USPcr-p] element transposon insertion. The resultant
fragment for each strain was directly sequenced to
determine the genomic sequence at the site of insertion.
Details of the protocols used can be found at
http://www.fruitfly.org/aiuoc/methods/inverse.pcr.html. *
15 a 7 c 11 g 6 t
BASE COUNT
ORIGIN
Query Match 13.3% Score 16: 0a 17: Length 39:
Best Local Similarity 68.8% Pred No. 3.9e-05:
Matches 22: Conservative 0: Mismatches 10: Indels 0: Gaps 0:
79 AATGATGATGGCTGCTCCATAGCTGGTAA 110
|||||
8 AAAAGACGAATCGAATCGAATGATGCTGAA 39
|||||

```

Genome Res. 6 (9), 807-828 (1996)	JOURNAL MEDLINE COMMENT	Genome Res. 6 (9), 807-828 (1996)	JOURNAL MEDLINE COMMENT
9704478	Contact: Wilton RK	9704478	Contact: Wilton RK
Washington University School of Medicine	4414 Forest Park Parkway, Box 8501, St. Louis, MO 63108	Washington University School of Medicine	4414 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800		Tel: 314 286 1800	
Fax: 314 286 1810		Fax: 314 286 1810	
Email: est@wustl.wustl.edu		Email: est@wustl.wustl.edu	
Insert Size: 794		Insert Size: 794	
High quality sequence starts: 1		High quality sequence starts: 1	
Source: IMAGE Consortium, LLNL This clone is available royalty-free		Source: IMAGE Consortium, LLNL This clone is available royalty-free	
through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)		through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)	
for further information.		for further information.	
Insert Length: 794		Insert Length: 794	
Seq primer: -21m13		Seq primer: -21m13	
High quality sequence stop: 1.		High quality sequence stop: 1.	
Location/Qualifiers		Location/Qualifiers	
1. 48		1. 48	
/organism="Homo sapiens"		/organism="Homo sapiens"	
/db_xref="GDB:497943"		/db_xref="GDB:497943"	
/db_xref="Taxon:9606"		/db_xref="Taxon:9606"	
/clone="IMAGE:78198"		/clone="IMAGE:78198"	
/clone_lib="Stratagene liver (#937224)"		/clone_lib="Stratagene liver (#937224)"	
/sex="male"		/sex="male"	
/dev_stage="49 years old"		/dev_stage="49 years old"	
/lab_host="SOLR cells (kanamycin resistant)"		/lab_host="SOLR cells (kanamycin resistant)"	
/note="Organ: Liver; Vector: pBluescript SK; Site: 1; ECORI"		/note="Organ: Liver; Vector: pBluescript SK; Site: 1; ECORI"	
; Site: 2; XhoI; Cloned unidirectionally. Primer: Oligo		; Site: 2; XhoI; Cloned unidirectionally. Primer: Oligo	
dt. Hepatectomy from normal male caucasian. Average insert		dt. Hepatectomy from normal male caucasian. Average insert	
size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5'		size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5'	
GAATTCGACGAG 3' -3' adaptor sequence: 5'		GAATTCGACGAG 3' -3' adaptor sequence: 5'	
CTCGAGTTTCTTTTCTTTT 3'		CTCGAGTTTCTTTTCTTTT 3'	
BASE COUNT	7 a 12 c 14 g 11 t	BASE COUNT	7 a 12 c 14 g 11 t
ORIGIN		ORIGIN	
Query Match	13.3%	Query Match	13.3%
Best Local Similarity	76.0%	Best Local Similarity	76.0%
Matches	19; Conservative	Matches	19; Conservative
	0; Mismatches		0; Mismatches
	6; Indels		6; Indels
	0; Gaps		0; Gaps
0; Gaps		0; Gaps	
Qy	6	Qy	6
Db	27	Db	27
	6 CCATAGTACCTCTTAACCCACA 30		6 CCATAGTACCTCTTAACCCACA 30
	11       11		11       11
	27 GCCATCTGCCCTCAACCGACA 3		27 GCCATCTGCCCTCAACCGACA 3
RESULT 24		RESULT 24	
AZ621474		AZ621474	
LOCUS		LOCUS	
DEFINITION		DEFINITION	
ACCESSION		ACCESSION	
VERSION		VERSION	
KEYWORDS		KEYWORDS	
SOURCE		SOURCE	
ORGANISM		ORGANISM	
Mus musculus		Mus musculus	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;	
1 (bases 1 to 50)		1 (bases 1 to 50)	
REFERENCE		REFERENCE	
AUTHORS		AUTHORS	
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,		Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,	
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,		Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,	
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,		M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,	
and Wright, D., Weigss, R.		and Wright, D., Weigss, R.	
Mouse whole genome scaffolding with paired end reads from 10kb		Mouse whole genome scaffolding with paired end reads from 10kb	
plasmid inserts		plasmid inserts	
Unpublished (2000)		Unpublished (2000)	
Contact: Robert B. Weiss		Contact: Robert B. Weiss	
University of Utah		University of Utah	
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT		Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT	
84112, USA		84112, USA	
Tel: 801 585 5606		Tel: 801 585 5606	
Fax: 801 585 7177		Fax: 801 585 7177	
Email: ddunn@genetics.utah.edu		Email: ddunn@genetics.utah.edu	
Insert Length: 10000		Insert Length: 10000	
Std Error: 0.00		Std Error: 0.00	
TITLE		TITLE	
JOURNAL		JOURNAL	
COMMENT		COMMENT	
TA994A100		TA994A100	
47 bp		47 bp	
DNA		DNA	
linear		linear	
GSS		GSS	
13-DEC-2000		13-DEC-2000	
T. brucei sheared genomic DNA clone 294a10, reverse sequence.		T. brucei sheared genomic DNA clone 294a10, reverse sequence.	
genomic survey sequence.		genomic survey sequence.	
AL486316		AL486316	
GI:11853377		GI:11853377	
GSS:		GSS:	
Trypanosoma brucei.		Trypanosoma brucei.	
Trypanosoma brucei.		Trypanosoma brucei.	
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;		Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;	
Trypanosoma		Trypanosoma	
1 (bases 1 to 47)		1 (bases 1 to 47)	

Plate: 0454 Row: O Column: C8  
Seq primer: CACACGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 50.  
Location/Qualifiers  
1. .50

## FEATURES

source

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0454008"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F."  
/note="Vector: pMD29v: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g11473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 12 a 2 c 10 g 26 t  
ORIGIN

Query Match 13.3% Score 16: DB 17: Length 50:

Best Local Similarity 88.8% Pred. No. 4.3e+05:

Matches 22: Conservative 0: Mismatches 10: Indels 0: Gaps 0:

QY 88 ATTGGCTTCATGCTGCTGAATTCGAGTTTA 119

DB 1 ATTGCTATATGATGCTGATATGATTTAA 32

## RESULT 25

A2806715/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

UNPUBLISHED (2000)

UNIVERSITY OF UTAH

GENOME CENTER

Rm. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0068 Row: O Column: 19  
Seq primer: CACACGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 50.  
Location/Qualifiers  
1. .50

## FEATURES

source

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0068019"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F."  
/note="Vector: pMD29v: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g11473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 6 c 18 g 18 t  
ORIGIN

Query Match 13.3% Score 16: DB 17: Length 50:

Best Local Similarity 62.5% Pred. No. 4.3e+05:

Matches 25: Conservative 0: Mismatches 15: Indels 0: Gaps 0:

QY 7 CCATAGTACCTCTCTACCCACACCTCATATATCCCACT 46

DB 46 CCATATCAGCATCCCAACACCTGACACCATTCATACACT 7

## RESULT 26

A2626127/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

UNPUBLISHED (2000)

UNIVERSITY OF UTAH

GENOME CENTER

Rm. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00









```

source
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="KAT11963"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
BASE COUNT      18 a   13 c   8 g   11 t
ORIGIN

Query Match      13.0%; Score 15.6; DB 9; Length 50;
Best Local Similarity 58.7%; Pred. NO. 5.8e+05;
Matches 27; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Oy 73 TCGTGAATGTCGATGCGTTCCTCATAGCTCTCGAATTCGAGTTT 118
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 50 TCGTGAATGTCGAGATGCGCTCAACGCTTAAAGCTTGGATGTGT 5

RESULT 31
AZ597958/c
LOCUS          50 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION    Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0412J23 F, DNA sequence.
ACCESSION     AZ597958
VERSION       AZ597958.1 GI:11720148
KEYWORDS      GSS.
SOURCE        house mouse.
ORGANISM      Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0412 row: J column: 23
Seq primer: CGTTGTAACAGCAGCGCCACT
Class: plasmid ends
High quality sequence stop: 50.
FEATURES
source
1. .50
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UUGC1M0412J23"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD22nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

```

```

of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance.
BASE COUNT      11 a   5 c   18 g   16 t
ORIGIN

Query Match      13.0%; Score 15.6; DB 17; Length 50;
Best Local Similarity 58.7%; Pred. NO. 5.8e+05;
Matches 27; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Oy 1 TCGATGCCATAGTACCTCTTACCCACACGCTCATATTCGCCACT 46
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 49 TCCATCCCAATATCATGCTTCCAAATGCTGACACCATCGCATACACT 4

RESULT 32
AZ776846
LOCUS          34 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION    Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0010A20 R, DNA sequence.
ACCESSION     AZ776846
VERSION       AZ776846.1 GI:12904831
KEYWORDS      GSS.
SOURCE        house mouse.
ORGANISM      Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0010 row: A column: 20
Seq primer: CACACAGGAACAGCATGACC
Class: plasmid ends
High quality sequence stop: 34.
FEATURES
source
1. .34
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UUGC2M0010A20"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD22nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

```







constructed by Zhao Bin and Wang Xianmei using pMD18-T vector. Randomly picked clones were sequenced at ABI 377 using M13R primer (ACGGATACAAATTCACAGG) by Wang Xianmei.  
9 a' Zhao Bin and Zhang Qian.  
9 a' 9 c 19 g 13 t

Query Match 12.8%; Score 15.4; DB 10; Length 50;  
Best Local Similarity 61.0%; Pred. No. 6.7e+05;

Matches 25; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 26 CCACACCTCATATCCCACTCCAGAGGATTCAGGGGTTTC 66  
II IIIIIII III IIIII III III III III III  
DB 43 CCGACCTCATGAGCCAGCCGCCAGGTAGCAAACTTTC 3

## RESULT 40

AW507292/c

LOCUS

EST007292 Plasmid Subtractive Library of Rat Cerebrum (stroke)

Rattus norvegicus cDNA clone 3rdC4, mRNA sequence.

ACCESSION

AW507292

VERSION

EST

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 50)

Zhu, X.M., Zhang, Q., Zhu, Z.M., Zhu, S.J. and Hui, R.T.

Cloning of Genes Responsible for Stroke

Unpublished (2000)

Other ESTs: EST00684

Contact: Bin Zhao

Molecular Medical Center for Cardiovascular Disease

Cardiovascular Institute, CAMS &amp; PUMC

167, Bei Li Shi Lu, 100037, Beijing, P.R. China

Tel: 86-10-68314466 ext 8136

Fax: 86-10-68313130

Email: binzhao@pwhua.com.cn

Seq primer: M13R

POLYA-No.

Location/Qualifiers

1..50

/organism="Rattus norvegicus"

/strain="Wistar"

/db\_xref="taxon:10116"

/clone="3rdC4"

/clone\_lib="Plasmid Subtractive Library of Rat Cerebrum (stroke)"

/sex="male"

/tissue\_type="Cerebrum"

/dev\_stage="8-12 weeks old"

/note="Vector: pMD18-T (Takara, D504 CA). The rat stroke model was developed by Wang Xianmei, Zhu Zhiming, Zhu Shanjun et al at 3rd Military Medical University Chongqing, China. The Suppression Subtraction Hybridization (SSH) was conducted at Fu Wai Hospital by Zhao Bin and Wang Xianmei in Beijing, China. Message RNA was extracted from pooled whole cerebrum from stroke and control rats respectively. SSH had been conducted following manufacture's manual using 5ug mRNA. The SSH library was constructed by Zhao Bin and Wang Xianmei using pMD18-T vector. Randomly picked clones were sequenced at ABI 377 using M13R primer (ACGGATACAAATTCACAGG) by Wang Xianmei and Zhang Qian."

9 a' 9 c 19 g 13 t

BASE COUNT

ORIGIN

Query Match 12.8%; Score 15.4; DB 10; Length 50;

Best Local Similarity 61.0%; Pred. No. 6.7e+05;

Matches 25; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

## OY

DB

RESULT 41

AW507292

LOCUS

DEFINITION

ACCESSION

AW507292

VERSION

KEYWORDS

SOURCE

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

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University of Utah

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Tel: 801 585 5606

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Email: ddunn@genetics.utah.edu

Insert Length: 10000

Plate: 0258

Seq primer: CACACAGGAACAGCATGACC

Class: plasmid ends

High quality sequence stop: 50.

Location/Qualifiers

1..50

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0258B20"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, P-"

/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g14732114g14732072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance.

0 a' 44 c 0 g 6 t

BASE COUNT

ORIGIN

Query Match 12.8%; Score 15.4; DB 17; Length 50;

Best Local Similarity 66.7%; Pred. No. 6.7e+05;

Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;



Journal Comment

plasmid inserts  
Unpublished (2000)  
Contacted: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
tel: 801 585 5606  
fax: 801 585 7177  
Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0171 row: G column: 12  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 45.

Location/Qualifiers	source
1. 45	
/organism="Mus musculus"	
/strain="C57BL/6J"	
/db_xref="taxon:10090"	
/clone="UGGCLM0171G12"	
/clone.lib="Mouse 10kb plasmid UUGCLM library"	
/sex="Male"	
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"	
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource ( <a href="http://www.jax.org/resources/documents/dnares/">http://www.jax.org/resources/documents/dnares/</a> ). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1147321141gb1Arl29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptorised mouse DNA was annealed to adaptorised vector DNA and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	

Query Match	12.7%	Score 15.2	DB 17	Length 45
Best Local Similarity	63.9%	Pred. No. 7.4e+05		
Matches 23	Conservative	0	Mismatches 13	Indels 0
Gap 0				
2	CGATGCCATAGTGACCGCTCTTAACCCACACACCTATT	37		
10	CCATCCCATATACATCTTCAAAACCCAGACACTATT	45		
RESULT 45				
AL758605/C				
LOCUS				
DEFINITION				
Arabidopsis thaliana T-DNA flanking sequence GK-160D11-013216,				
genomic survey sequence.				
AL758605				
AL758605				
1	GI:21496953			
GSS.				
SOURCE				
thale cress,				
ORGANISM				
Arabidopsis thaliana				
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:				
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:				
Rosidae: eurosids II: Brassicales: Brassicaceae: Arabidopsis.				
1				
REFERENCE				
AUTHORS				
Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.				
and Weishaar,B.				
TITLE				
A pipeline for automated high-throughput generation of ESTs				
(flanking sequence tags) from Arabidopsis thaliana T-DNA				

JOURNAL REFERENCE AUTHORS TITLE	transformed lines unpublished
JOURNAL REFERENCE AUTHORS TITLE	2 Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weissshaar, B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
JOURNAL REFERENCE AUTHORS TITLE	3 (bases 1 to 45) Strizhov, N., Rosso, M., Li, Y. and Weissshaar, B. Direct Submission
JOURNAL REFERENCE AUTHORS TITLE	Submitted (17-JUN-2002) Weissshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone F14K14. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <a href="http://www.molgen.mpg.de/GABI-Kat/">http://www.molgen.mpg.de/GABI-Kat/</a>
COMMENT	

```

FEATURES
  source          1.. 45
    Location/Qualifiers
      1.. 45
      /organism="Arabidopsis thaliana"
      /strain="Columbia 0"
      /db_xref="taxon:3702"
      /clone="GK-160D11-013216"
      /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
      /notes="PCR was performed on DNA from Arabidopsis thaliana
      (Ti) which were transformed with the T-DNA from
      vector pAC161. The lines contain one or more T-DNA
      insertions. The DNA fragment(s) resulting from the PCR
      were directly sequenced to determine the genomic sequence
      flanking the insertion. Sequences displaying significant
      similarity to the A. thaliana nuclear genome sequence were
      processed for submission. T-DNA derived sequences were
      removed."
      16 a      11 c      5 g      13 t
      BASE COUNT
      ORIGIN
        Query Match      12.74; Score 15.2; DB 17; Length 45;
        Best Local Similarity 71.44; Pred. No. 7.4e+05;
        Matches 20; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
        91 GCCTTCATAGCTGCTGAATTCAGTTT 118
           11 111 111111 11111 1111
        36 GGATTCATAGCTGAATTCAGTTT 9
           11 111 111111 11111 1111

```

RESULT 46  
 AB026579/c  
 LOCUS  
 DEFINITION  
 46 bp mRNA linear. EST 24-FEB-1998  
 c06910.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA clone IMAGE:1415642 3'.  
 similar to SW:ASHJ\_HUMAN P30553 ACHAETE-SCUTE HOMOLOG 1. : contains  
 element LTR4 repetitive element ; mRNA sequence.  
 AB026579  
 Accession  
 Version  
 Keywords  
 EST  
 AB026579.1 GI:2898406  
 human.  
 SOURCE  
 Homo sapiens  
 Organism  
 Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 46)  
 NCI\_CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: [ncicgap-clone.distribution@nih.gov](mailto:ncicgap-clone.distribution@nih.gov)



found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.lnl.gov/nbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40ml fwd, 57 from Amersham  
High quality sequence stop: 1

## FEATURES

Source  
1..46  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1416642"  
/clone\_lib="MCL CGAP.Lu5"  
/tissue\_type="carcinoid"  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptor (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

## BASE COUNT

13 a 14 c 14 g 5 t  
Query Match 12.7% Score 15.2; DB 9; Length 46;  
Best Local Similarity 71.4% Pred. No. 7.5e+05;  
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
Oy 85 TCGATGCTTCATAGCGTGGTGAATTG 112  
Db 43 TCGCTGACTGCTGGCGCTGACTTG 16

## RESULT 47

AL762625/c  
LOCUS  
DEFINITION  
HATH heat shock1 final cluster121(2) DMC1s Homo sapiens cDNA  
similar to ribosomal protein S27, mRNA sequence.  
ACCESSION  
AL762625.1 GI:6651953  
VERSION  
AL762625.1  
KEYWORDS  
EST.  
SOURCE  
human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 47)  
Brenner, S., Williams, S.R., Vermaas, E.H., Stoick, J., Moon, K.,  
McCollum, C., Mao, J.I., Kirchner, J.J., Eletre, S., DuBridge, R.B.,  
Burcham, T. and Albrecht, G.  
In vitro cloning of complex mixtures of DNA on microbeads: Physical  
separation of differentially expressed cDNAs  
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

## JOURNAL

20144098  
Contact: Burcham TS  
LYNX Therapeutics, Inc.  
25861 Industrial Blvd., Hayward, CA 94545, USA  
Tel: 510 670 9338  
Fax: 510 670 9302  
Email: timbel@lynxgen.com  
Sequence obtained from LYNX Therapeutics Megasort technology.  
Collected from the down-regulated gate. Consensus sequence of 2  
sequences in cluster.  
High quality sequence stop: 47.

## FEATURES

Source  
1..47  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="DMC1S"  
/cell\_type="monocytic leukemia"  
/cell\_line="THP-1 (71B-202)"  
/note="Vector: PCR2.1. Cloning of PCR products from micro-beads carrying 3' end of down-regulated cDNA. THP-1

BASE COUNT 18 a 12 c 10 g 7 t  
Origin  
cells non-induced (treated with DMSO only)."

Query Match 12.7% Score 15.2; DB 10; Length 47;  
Best Local Similarity 63.9% Pred. No. 7.5e+05;  
Matches 23; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Oy 31 CCTCATTTATCCCACTCCAGAGGATTCAGCGCTTC 66  
Db 36 CCTCTTCTCTCTCTCTGGAGGAGGATGAAGGATC 1

## RESULT 48

AL656975  
LOCUS  
DEFINITION  
AL656975 XGC-neurula Silurana tropicalis cDNA clone TNeu033k22 5',  
mRNA sequence.

ACCESSION  
AL656975  
VERSION  
AL656975.1 GI:17564540  
KEYWORDS  
EST.  
SOURCE  
western clawed frog.

## ORGANISM

Silurana tropicalis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
Xenopodinae; Silurana.  
1 (bases 1 to 48)  
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.J.  
Sanger Xenopus tropicalis EST project 2001 (10\_2001)  
Unpublished (2001)  
Contact: Huckle E.  
Sanger Centre  
Hinxton, Cambridgeshire, CB10 1SA, UK

## REFERENCE

1  
Sanger Xenopus tropicalis EST project 2001  
THOPICALIS\_SEQUENCE\_ID: TNeu033k22.sp6  
Sequencing primer: SP6  
This sequence is from a Xenopus Gene Collection (XGC) library  
constructed by Aaron M. Zorn.  
Location/Qualifiers  
1..48  
/organism="Silurana tropicalis"  
/db\_xref="taxon:8364"  
/clone="TNeu033k22"  
/clone\_lib="XGC-neurula"  
/lab\_host="Escherichia coli DH10B"  
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA  
was oligo dT primed from Sug of poly A+ RNA from neurula.  
EcoRI-NotI cut cDNA was then ligated into pCS107 with  
EcoRI at the 5' end and NotI at the 3' end."

## FEATURES

Source  
1..48  
/organism="Silurana tropicalis"  
/db\_xref="taxon:8364"  
/clone="TNeu033k22"  
/clone\_lib="XGC-neurula"  
/lab\_host="Escherichia coli DH10B"  
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA  
was oligo dT primed from Sug of poly A+ RNA from neurula.  
EcoRI-NotI cut cDNA was then ligated into pCS107 with  
EcoRI at the 5' end and NotI at the 3' end."

## BASE COUNT

14 a 7 c 10 g 17 t  
Query Match 12.7% Score 15.2; DB 9; Length 48;  
Best Local Similarity 71.4% Pred. No. 7.6e+05;  
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 53 GGATTCAGGGGTTCCAGCGTTCCTGAAA 80  
Db 14 GCTTTCACGGATTTAACACATTCGTGAAA 41

## RESULT 49

AL762625/c  
LOCUS  
DEFINITION  
Arabidopsis thaliana T-DNA flanking sequence GR-026F02-013727,  
genomic survey sequence.

ACCESSION  
AL762625  
VERSION  
AL762625.1 GI:21509033  
KEYWORDS  
GSS.  
SOURCE  
thale cress.

## ORGANISM

Arabidopsis thaliana  
Eukaryota; Embryophyta; Angiosperms; Brassicales; Brassicaceae; Arabidopsis  
1..48  
/organism="Arabidopsis thaliana"  
/db\_xref="taxon:10116"  
/clone\_lib="GSS"  
/cell\_type="thale cress"  
/cell\_line="GSS"  
/note="T-DNA flanking sequence GR-026F02-013727, genomic survey sequence."







```

FEATURES
  source
    High quality sequence stop: 50.
    Location/Qualifiers
      1..50
        /organism="Mus musculus"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC1M0009N10"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
        /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
      9 a 11 c 11 g 19 t
      BASE COUNT
      9 a 11 c 11 g 19 t

  Query Match 12.74; Score 15.2; DB 17; Length 50;
  Best Local Similarity 63.94; Pred. No. 7.8e+05;
  Matches 23; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

  QY 49 AGAGGATTCAGGGCTTCCAGCGCTTCCTGAAATGA 84
      ||| ||| ||| ||| ||| ||| ||| ||| |||
  DB 15 AAGTCATGCTGACCTTCTGCTTCTCTGTAATGA 50

  RESULT 55
  AA908637/c
  LOCUS
  DEFINITION
  Similar to TR:099495 099495 DRPLA PROTEIN. ; mRNA sequence.
  ACCESSION
  AA908637
  VERSION
  AA908637.1
  KEYWORDS
  EST.
  SOURCE
  human.
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
  1 (bases 1 to 25)
  NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap.
  National Cancer Institute, Cancer Genome Anatomy Project (CCAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs@mail.nih.gov
  Trace considered overall poor quality
  Seq primer: -40ml3 fwd. ET from Amersham
  High quality sequence stop: 1.
  Location/Qualifiers
    1..25
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:145205"
      /clone.lib="NCI-CCAP-Ov8"
      /tissue_type="serous adenocarcinoma"
      /lab_host="DH108"
      /note="Organ: ovary; Vector: pCMV-SPORT4; Site_1: SalI;

FEATURES
  source
    Site_2: Not1: Cloned unidirectionally. Primer: Oligo dt.
    Average insert size 1.1 kb. Life technologies catalog #:
    10982-015"
    5 a 0 c 17 g 2 t 1 others
    BASE COUNT
    5 a 0 c 17 g 2 t 1 others
    ORIGIN
    Query Match 12.54; Score 15; DB 9; Length 25;
    Best Local Similarity 75.04; Pred. No. 6.6e+05;
    Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

  QY 25 CCACACCTCATTATCCACACCTCC 48
      ||||| ||| ||| ||||| |||
  DB 25 CCACCCGCTTTTCCCCACC 2

  RESULT 56
  AZ636460/c
  LOCUS
  DEFINITION
  33 bp DNA linear GSS 13-DEC-2000
  Clone UUGC1M0495M14 F, DNA sequence.
  ACCESSION
  AZ636460
  VERSION
  AZ636460.1
  KEYWORDS
  GSS.
  SOURCE
  house mouse.
  ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 33)
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
  M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
  and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: dunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0495 row: M column: 14
  Seq primer: CGTGTAAACGACGGCCACT
  Class: plasmid ends
  High quality sequence stop: 33.
  Location/Qualifiers
    1..33
      /organism="Mus musculus"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0495M14"
      /clone.lib="Mouse 10kb plasmid UUGC1M library"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
      /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 8 a 0 c 18 g 7 t

Query Match 12.5% Score 15: DB 17: Length 33:  
Best Local Similarity 57.7%: Pred. No. 7.5e+05;  
Matches 21: Conservative 0: Mismatches 10: Indels 0: Caps 0:

Qy 17 CCTCTAACCCACACTTCATTCGCCACTC 47  
D6 31 CCCACTATACACACCTTTCTACCCGCCACC 1

RESULT 57  
AZ380286/c  
LOCUS  
DEFINITION  
1M0136E12F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
clone UUGCLM0136E12 F, DNA sequence.

ACCESSION  
AZ380286  
VERSION  
KEYWORDS  
SOURCE  
house mouse.

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
1 (bases 1 to 34)  
Dunn, D., Ayagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly  
and Wright, D., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0136 row: E column: 12  
Seq primer: CGTTGTAACACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 34.  
Location/Qualifiers

FEATURES  
source  
1..34  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCLM0136E12"  
/clone\_lib="Mouse 10kb plasmid UUGCLM library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
/notes="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (314732143614912972), a copy-number  
inducible derivative of plasmid p1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 6 a 4 c 13 g 11 t

Query Match 12.5% Score 15: DB 17: Length 34:  
Best Local Similarity 67.7%: Pred. No. 7.6e+05;  
Matches 21: Conservative 0: Mismatches 10: Indels 0: Caps 0:

Qy 7 CCATAGTACCCCTCTTAACCCACACCTCAT 37  
D6 33 CCATATCATCATCCACACGCTGACACCAT 3

RESULT 58  
AZ659063/c  
LOCUS  
DEFINITION  
1M0536N10F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
clone UUGCLM0536N10 F, DNA sequence.

ACCESSION  
AZ659063  
VERSION  
KEYWORDS  
SOURCE  
house mouse.

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
1 (bases 1 to 36)  
Dunn, D., Ayagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly  
and Wright, D., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0536 row: N column: 10  
Seq primer: CGTTGTAACACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 36.  
Location/Qualifiers

FEATURES  
source  
1..36  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCLM0536N10"  
/clone\_lib="Mouse 10kb plasmid UUGCLM library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
/notes="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (314732143614912972), a copy-number  
inducible derivative of plasmid p1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

```

BASE COUNT      10 a      6 c      8 g      12 t
ORIGIN
Query Match      12.5%   Score 15;   DB 17;   Length 36;
Best Local Similarity 67.7%   Pred. No. 7.8e+05;
Matches 21: Conservative 0: Mismatches 10: Indels 0: Gaps 0:

```

RESULT 59					
AZ309443					
LOCUS					
DEFINITION					
AZ309443	42 bp	DNA	linear	GSS 29-SEP-2000	
IM001301LR	Mouse 10kb plasmid	UUCGCM library	Mus musculus genomic		
clone UUCGCM001301L	R.	DNA sequence.			

ACCESSION	AZ09443				
VERSION	AZ09443.1	GI:10350430			
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Mammalia: Eutheria: Rodentia: Muridae: Musinae: Mus.  
 1 (bases 1 to 42)  
 Dunn, D., Aoyagi, A., Barber, M., Beccorn, T., Duval, B., Hamil, C.,  
 Istan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Relly  
 M., Rose, N., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,  
 and Wright, D., Weiss, R.

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weigs

FEATURES	Location/Qualifiers
source	1. .42

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

```

BASE COUNT      7 a      19 c      6 g      10 t
ORIGIN

Query Match      12.5%   Score 15;   DB 17;   Length 42;
Best Local Similarity 67.7%   Pred. NO. 8.3e+05;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```

[illegible]

ACCESSION A1937592  
VERSION A1937592.1 GI:5676462  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

**REFERENCE**  
**AUTHORS**  
**TITLE**

Eukaryote, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi: Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 46)  
NCI/NINDS-GAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGA), Tumor Gene Index

JOURNAL  
COMMENT

Trace considered overall poor quality  
Insert length: 702 Std Error: 0.00  
Seq primer: -40up from gibco  
High quality sequence stop: 1.  
Location/Qualifiers:

BASE COUNT	8 a	15 c	11 g	12 t
ORIGIN	Soares and M. Fatima Bonaloo.			

OY 80 AATGATCGATTGGCTCCATAGCTGCTGAAT 110  
 DB 2 AATATCTTTGGCTCCACACTGCTGCAT 32

RESULT 61  
 A2579592  
 LOCUS 47 bp DNA linear GSS 13-DEC-2000  
 DEFINITION 1M0367002F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
 accession A2579592  
 version A2579592  
 keywords GSS:11694021  
 source Mouse mouse  
 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 47)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,  
 and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0367 Row: 0 Column: 02  
 Seq primer: CGTGTAAACAGCCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 47.  
 Location/Qualifiers  
 1  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGCLM0367002"  
 /clone.lib="Mouse 10kb plasmid UUGCLM library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F."  
 /note="Vector: pMD22nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD22 (gil473211419b1AP129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 16 a 4 c 12 g 15 t  
 ORIGIN  
 Query Match 12.5% Score 15; DB 17; Length 47;  
 Best Local Similarity 57.7% Pred No. 8 Be+05;  
 Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 33 TCATTATCCCACTCCAGAGGATTCAGGGG 63  
 DB 7 TCATTTCACAAATTTCAGAGGATTCAGGGG 37

RESULT 62  
 A2768567  
 LOCUS 47 bp DNA linear GSS 16-FEB-2001  
 DEFINITION 1M0368005R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
 accession A2768567  
 version A2768567  
 keywords GSS:12887646  
 source Mouse mouse  
 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 47)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,  
 and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0368 Row: 0 Column: 05  
 Seq primer: CACACAGCAACACCTAGACC  
 Class: plasmid ends  
 High quality sequence stop: 47.  
 Location/Qualifiers  
 1  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGCLM0568005"  
 /clone.lib="Mouse 10kb plasmid UUGCLM library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F."  
 /note="Vector: pMD22nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD22 (gil473211419b1AP129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 17 a 13 c 7 g 10 t  
 ORIGIN  
 Query Match 12.5% Score 15; DB 17; Length 47;  
 Best Local Similarity 76.3% Pred No. 8 Be+05;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

QY 60 GGGTTCCAGGCTTCCTGAAAT 82
DB 24 GGTGTCTCAGGCTTCCTGGAAT 2

RESULT 63
LOCUS BH849286
DEFINITION Arabidopsis thaliana genomic clone SALK_069476.34.50.n, DNA
sequence.
ACCESSION BH849286
VERSION BH849286.1 GI:21420157
KEYWORDS GSS:
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Cadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
,Zimmerman,J. and Eckert,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Arabidopsis Genome
COMMENT Unpublished (2001)
Contact: Joseph R. Eckert
The Salk Institute Genomic Analysis Laboratory (SIGAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckert@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 3' end of
At4g22150.
Class: TDNA tagged.
FEATURES
Location/Qualifiers
SOURCE 1..47
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_069476.34.50.n"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/Note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"
BASE COUNT 16 a 5 c 10 g 16 t
ORIGIN
Query Match 12.5% Score 15; DB 17; Length 47;
Best Local Similarity 78.3%; Pred. No. 8.8e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 73 TCTGAAATGATCGATGCGCT 95
DB 4 TACTGAAATATTCATCGCGCT 26

RESULT 64
LOCUS AU102397
DEFINITION AU102397 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
sequence.
ACCESSION AU102397
VERSION AU102397.1 GI:13551917
KEYWORDS EST:
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Primates; Catarrhini; Hominidae; Homo.
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
H., Oka,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
Location/Qualifiers
SOURCE 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CAS09317"
/clone_lib="Sugano Homo sapiens CDNA library"
/Note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
BASE COUNT 10 a 15 c 14 g 11 t
ORIGIN
Query Match 12.5% Score 15; DB 9; Length 50;
Best Local Similarity 78.3%; Pred. No. 9e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 52 GGGATTCCAGGCTTCAGCGCTTC 74
DB 50 GGGAGCCAGAGGTTCCAGTGATC 28

RESULT 65
LOCUS AU102413
DEFINITION AU102413 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
sequence.
ACCESSION AU102413
VERSION AU102413.1 GI:13551933
KEYWORDS EST:
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
H., Oka,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
Location/Qualifiers
SOURCE 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CAS09317"
/clone_lib="Sugano Homo sapiens CDNA library"
/Note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"

```











2000-2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

```

BASE COUNT      12 a      9 c      11 g      15 t
ORIGIN
Query Match      12.3%   Score 14.8:  DB 17:  Length 47;
Best Local Similarity 64.7%;  Pred. No. 1e+06;
Matches 22: Conservative 0: Mismatches 12: Indels 0: Gaps 0:

```

56 **TT**CAGGGG**TT**CCAGCG**TT**CCTGAA**AA**TGATCGAT 89  
||||| ||| | ||| ||||| |||  
13 **TT**CAGATG**TT**GAA**TT**CCATCAT**GT**GCCATGATGGAT 46

RESULT 73	AZ442808	48 bp	DNA	linear	GSS 04-OCT-2000
LOCUS					
DEFINITION					
	AZ442808	48 bp	DNA	linear	GSS 04-OCT-2000
	1M0237N08F	Mouse 10kb plasmid	UUGC1M library	Mus musculus	genomic
	clone UUGC1M0237N08 F.	DNA sequence.			

ACCESSION AZ442808  
VERSION AZ442808.1 GI:10590177  
KEYWORDS GSS.

SOURCE	ORGANISM
house mouse.	Mus musculus.
	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
	Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae; Mus.
REFERENCE	1 (bases 1 to 48)

**AUTHORS**  
Dunn, D., Aoyagi, A., Barber, M., Becorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.,  
and Wright, R., Weiss, R.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

**JOURNAL  
COMMENT**

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunen@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0237 row: N column: 08  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 48.

Location/Qualifiers	Source
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/organism="Mus musculus"	
/strain="C57BL/6J"	
/db_xref="taxon:10090"	
/clone="U00C1M0237N08"	
/clone_lib="Mouse 10kb plasmid U00C1M library"	
/sex="Male"	
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"	
/note="vector: PMO42v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource ( <a href="http://www.jax.org/resources/documents/dnares/">http://www.jax.org/resources/documents/dnares/</a> )". The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g3147321141gb1AF120972.1), a copy-number inducible derivative of plasmid p1. The vector was ligated with adaptors complementary to the insert adaptors and	

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* X10-Gold (Stratagene) cells and selected for ampicillin resistance.

```

BASE COUNT      12 a      16 c      5 g      15 t
ORIGIN
Query Match      12.3%      Score 14.8      DB 17      Length 48;
Best Local Similarity 73.1%      Pred. No. 1e-06;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

24 ACCCACCTCATTTATCCCACTCCA 49  
13 ACCCATATCTCATATGACCCCTCTCCA 38

RESULT 74
AZ6233464/C
LOCUS
DEFINITION
AZ6233464
48 bp DNA linear
GSS 13-DEC-2000
1M0461F15F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0461P15 F. DNA sequence.

ACCESSION A2623404  
VERSION A2623464.1 GI:11745654  
KEYWORDS GSS.

SOURCE	ORGANISM
house mouse.	<i>Mus musculus</i>
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE	1 (bases 1 to 48)

**AUTHORS**  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, N., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.,  
and Wright, D. Weiss, R.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT

Tel.: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 plate: 0461 row: F column: 15  
 Seq primer: CGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence step: 48

Location/Qualifiers	Source
1. 48	
/organism="Mus musculus"	
/strain="C57BL/6J"	
/db_xref="taxon:10090"	
/clone="UUGC1M0461F15"	
/clone_lib="Mouse 10kb plasmid WUGC1M library"	
/sex="Male"	
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"	
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource ( <a href="http://www.jax.org/resources/documents/dnares/">http://www.jax.org/resources/documents/dnares/</a> ). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adoped DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gii47321141gb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and	







JOURNAL  
MEDLINE  
COMMENT

Genome Res. 6 (9), 807-828 (1996)

Contact: Wilson RK  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estevenson.wustl.edu

This clone is available royalty-free through LNL : contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.

Seq primer: reverse ET

High quality sequence stop: 1.

FEATURES  
source

1. .39  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="GDB:3866225"  
/db\_xref="taxon:9606"  
/clone="IMAGE:25816"  
/clone\_lib="Weizmann Olfactory Epithelium"  
/sex="Female"  
/tissue\_type="olfactory epithelium"  
/dev\_stage="35 year old"  
/lab\_host="SOLR cells (kanamycin resistant)"  
/note="Organ: nose; Vector: pBluescript SK-; Site: 1: EcoRI  
Site 2: XhoI; Cloned unidirectionally. Primer: Oligo  
dT; Olfactory epithelium, normal. Average insert size: 0.8  
kb; Uni-ZAP XR Vector. Library constructed by N. Walker,  
D. Lencet, Weizmann Institute of Science. -5' adaptor  
sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5'  
CTCAGTGTGTTTTTTTTTTT 3'.

BASE COUNT 11 a 9 c 10 g 7 t 2 others

Query Match 12.2% Score 14.6; DB 14; Length 39;

Best Local Similarity 64.5%; Pred. NO. 1.1e+06;

Matches 20; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 85 TCGATTGCTTCATCTGCTGAATTCGAG 115

DB 34 TTGTCAGTCCCTGAGTACGTCGATTACAG 4

RESULT 83  
A2650740/c

LOCUS A2650740 39 bp DNA linear GSS 14-DEC-2000  
DEFINITION IM0521N05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0521N05 F, DNA sequence.

ACCESSION A2650740

VERSION A2650740.1 GI:11785531

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 39)

AUTHORS Dunn.D., Aoyagi.A., Barber.M., Beacorn.T., Duval.B., Hamil.C.,

Islam.H., Longacre.S., Mahmood.M., Meenen.E., Pedersen.T., Rellly

, M., Rose.N., Rose.R., Stokes.R., Tingey.A., von Niederhausen,A.

and Wright.D., Weiss.R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Em. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0521 row: N column: 05

Seq primer: CCGTGTAAACGACGCCAGT

FEATURES  
source

Class: plasmid ends  
High quality sequence stop: 39.  
Location/Qualifiers  
1. .39  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0521N05"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Cold, T1-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (G1473211419b) AFI29072.11, a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance.

BASE COUNT 11 a 0 c 25 g 3 t

Query Match 12.2% Score 14.6; DB 17; Length 39;

Best Local Similarity 69.0%; Pred. NO. 1.1e+06;

Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 20 CCTACCCACACCTCATTCCTCCACTCC 48

DB 38 CCTCCCTCTCTCCATTACCTCCCTCC 10

RESULT 84  
A1351416

LOCUS A1351416 43 bp mRNA linear EST 13-FEB-1999  
DEFINITION q37h01.x1 Soares\_total\_fetus\_M02HF8\_3w Homo sapiens cDNA clone  
IMAGE:1934737 3' similar to SW:EBN2\_EBV P12978 EBNA-2 NUCLEAR  
PROTEIN. [1] ;, mRNA sequence.

ACCESSION A1351416

VERSION A1351416.1 GI:4088622

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 43)

AUTHORS NC1-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

This clone is available royalty-free through LNL : contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1053 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. .43

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1934737"





was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114/gb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 19 a 8 c 6 g 13 t  
 Query Match 12.24; Score 14.6; DB 17; Length 46;  
 Best Local Similarity 81.04; Pred. No. 1.2e+06;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 78 AAATGATCGATGGCTTCA 98  
 DB 26 AAATGATCGATGGCTTCA 46

## RESULT 87

C21077/c  
 LOCUS C21077 49 bp mRNA linear EST 23-OCT-1996  
 DEFINITION HUMG0002591 Human adult (X.Okubo) Homo sapiens cDNA 3', mRNA sequence.  
 ACCESSION C21077  
 VERSION C21077.1 GI:1622187  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Okubo, K.  
 BodyMap: human gene expression database  
 Unpublished (1995)  
 Contact: Okubo, K.  
 Institute for Molecular and Cellular Biol  
 Osaka University  
 1-3 Yanada-oka, Suita, Osaka Pref. 565, Japan  
 Tel: 06-877-5111 (ex.3315)  
 Email: kousuke@imcb.osaka-u.ac.jp

Human Gene Signature, 3'-directed cDNA sequence. We are not submitting the same cDNA sequence redundantly to DBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see <http://www.imcb.osaka-u.ac.jp/bodymap/>. The sequences of the clones represented by this GS sequences is also found there.  
 Location/Qualifiers  
 1..49  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Human adult (K.Okubo)"  
 /dev\_stage="adult"  
 /note="Organ: blood; Vector: l-gt-11; Site1: Eco-RI; Monoclonal were prepared from blood by ficoll-hyphaque, percoll and T cell rosetting purification steps (purity: 96 %). mRNA was prepared from activated monocytes from a patient with rheumatoid arthritis. mRNA was reverse transcribed with MULV, using Eco-RI linkers cDNA was cloned into l-gt-11 vector arms. The cDNA library was screened by differential hybridization using radioactively marked ss-cDNA from activated and non-activated monocytes.

## FEATURES

source  
 12 a 16 c 10 g 11 t

## BASE COUNT

ORIGIN  
 Query Match 12.24; Score 14.6; DB 14; Length 49;

Best Local Similarity 57.84; Pred. No. 1.2e+06;  
 Matches 20; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
 QY 17 CCTCTAACCACACCTCATTTATCCCTACTCCAGAGGATTCAGG 61  
 DB 48 CCTGTGAAATGCACCTTTATTTGCTCCCGAGGAGTGGATTCAGG 4

## RESULT 88

AU102946/c  
 LOCUS AU102946 50 bp mRNA linear EST 30-AUG-2001  
 DEFINITION AU102946 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone ADS01729, mRNA sequence.  
 ACCESSION AU102946  
 VERSION AU102946.1 GI:13552467  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 50)  
 AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites  
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
 MEDLINE 21270072  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: ysuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.  
 S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

## FEATURES

source  
 1..50  
 Location/Qualifiers  
 6 a 20 c 16 g 8 t  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Sugano Homo sapiens cDNA library"  
 /note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"

## BASE COUNT

ORIGIN  
 Query Match 12.24; Score 14.6; DB 9; Length 50;  
 Best Local Similarity 62.24; Pred. No. 1.2e+06;  
 Matches 23; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 42 CCATCCACAGGATTCAGGGTTCACGGTTCCTGA 78  
 DB 43 CCACAGCATGGCTGCGCGCGCGTGCAGGTCCTCCGA 7

## RESULT 89

AU108029/c  
 LOCUS AU108029 50 bp mRNA linear EST 30-AUG-2001  
 DEFINITION AU108029 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone KAIA2267, mRNA sequence.  
 ACCESSION AU108029  
 VERSION AU108029.1 GI:13557551  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 50)  
 AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites  
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: ysuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.  
 S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

JOURNAL  
MEDLINE  
COMMENT

mapping of mRNA start sites  
EMBO Rep. 2 (5), 368-395 (2001)  
21270072  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusukif@u-tokyo.ac.jp  
Suzuki, Y., Yoshitomo Nakagawa, et al.  
Construction and characterization of a full length cDNA and  
a 5'-end enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

## FEATURES

Source  
/organism="Mus musculus"  
/db\_xref="taxon:9606"  
/clone="VAT1267"  
/clone.lib="Sugano Homo sapiens cDNA library"  
/note="Differential display comparison of untreated and  
dimethylformate treated U937 cells"

BASE COUNT 7 a 16 c 15 g 12 t  
ORIGIN

Query Match 12.2% Score 14.6; DB 9; Length 50;  
Best Local Similarity 81.0%; Pred. No. 1.2e-06;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 86 CGATTGGCTTCACGCTGCT 106  
Db 30 CGATTGGCTTCACGCTGCT 50

RESULT 90  
AZ416047 50 bp DNA linear GSS 03-OCT-2000  
LOCUS  
DEFINITION  
1M019121IF Mouse 10kb plasmid UUCIM library Mus musculus genomic  
clone UUCIM1019121 F, DNA sequence.

ACCESSION  
AZ416047  
VERSION  
GSS.

KEYWORDS  
SOURCE  
house mouse.

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu

REFERENCE  
1 (bases 1 to 50)  
Plate: 0191 row: E, column: 11  
Seq primer: CGTTGTAACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 50.

FEATURES  
Source  
Location/Qualifiers  
1..50 on/Qualifiers  
/organism="Mus musculus"  
/db\_xref="taxon:9606"  
/clone="VAT1267"  
/clone.lib="Sugano Homo sapiens cDNA library"  
/note="Differential display comparison of untreated and  
dimethylformate treated U937 cells"

BASE COUNT 7 a 16 c 15 g 12 t  
ORIGIN

Query Match 12.2% Score 14.6; DB 9; Length 50;  
Best Local Similarity 81.0%; Pred. No. 1.2e-06;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 86 CGATTGGCTTCACGCTGCT 106  
Db 30 CGATTGGCTTCACGCTGCT 50

RESULT 90  
AZ416047 50 bp DNA linear GSS 03-OCT-2000  
LOCUS  
DEFINITION  
1M019121IF Mouse 10kb plasmid UUCIM library Mus musculus genomic  
clone UUCIM1019121 F, DNA sequence.

ACCESSION  
AZ416047  
VERSION  
GSS.

KEYWORDS  
SOURCE  
house mouse.

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu

REFERENCE  
1 (bases 1 to 50)  
Plate: 0191 row: E, column: 11  
Seq primer: CGTTGTAACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 50.

FEATURES  
Source  
Location/Qualifiers  
1..50 on/Qualifiers  
/organism="Mus musculus"  
/db\_xref="taxon:9606"  
/clone="VAT1267"  
/clone.lib="Sugano Homo sapiens cDNA library"  
/note="Differential display comparison of untreated and  
dimethylformate treated U937 cells"

BASE COUNT 7 a 16 c 15 g 12 t  
ORIGIN

Query Match 12.2% Score 14.6; DB 9; Length 50;  
Best Local Similarity 81.0%; Pred. No. 1.2e-06;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 86 CGATTGGCTTCACGCTGCT 106  
Db 30 CGATTGGCTTCACGCTGCT 50

RESULT 91  
AA868967/c 34 bp mRNA linear EST 04-JAN-1999  
LOCUS  
DEFINITION  
3' similar to SM7524\_MOUSE P5395 PROTEIN TSG24. mRNA sequence.

ACCESSION  
AA868967  
VERSION  
EST.

KEYWORDS  
SOURCE  
human.

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps@mail.nih.gov  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.htm

/note="Vector: pMD22v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/). The DNA was hydrolytically sheared by repeated passage through a 0.805 inch orifice at constant DNA velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 ligase. The blunt ends were ligated with high efficiency adapters. The ligated DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. The DNA was prepared from a derivative of pMD22 (9.5/173214101AF125072) (5' copy number) with adapters complementary to the insert adapters and purified. The sheared adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 15 a 10 c 15 g 10 t  
ORIGIN

Query Match 12.2% Score 14.6; DB 17; Length 50;  
Best Local Similarity 59.0%; Pred. No. 1.2e-06;  
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 8 CATAGTCACCTCTCAACCCACACCTCAT 36  
Db 34 CATAGTCGCTGCTAGCCCTCACTTAT 6

RESULT 91  
AA868967/c 34 bp mRNA linear EST 04-JAN-1999  
LOCUS  
DEFINITION  
3' similar to SM7524\_MOUSE P5395 PROTEIN TSG24. mRNA sequence.

ACCESSION  
AA868967  
VERSION  
EST.

KEYWORDS  
SOURCE  
human.

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps@mail.nih.gov  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.htm

REFERENCE  
1 (bases 1 to 34)  
Seq primer: -40m3 fwd: Et from Amerisham  
High quality sequence stop: 1.  
Location/Qualifiers  
1..34 on/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:140910"  
/clone.lib="Soares\_cstis\_MHT"  
/sex="male"  
/lab\_host="DH10B"  
/note="Vector: pT730-pac (Pharmacia) with a modified  
polylinker. Site\_1: Not 1; Site\_2: Eco RI; 1st strand cDNA

BASE COUNT 15 a 10 c 15 g 10 t  
ORIGIN

Query Match 12.2% Score 14.6; DB 17; Length 50;  
Best Local Similarity 59.0%; Pred. No. 1.2e-06;  
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 8 CATAGTCACCTCTCAACCCACACCTCAT 36  
Db 34 CATAGTCGCTGCTAGCCCTCACTTAT 6

RESULT 91  
AA868967/c 34 bp mRNA linear EST 04-JAN-1999  
LOCUS  
DEFINITION  
3' similar to SM7524\_MOUSE P5395 PROTEIN TSG24. mRNA sequence.

ACCESSION  
AA868967  
VERSION  
EST.

KEYWORDS  
SOURCE  
human.

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps@mail.nih.gov  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.htm

REFERENCE  
1 (bases 1 to 34)  
Seq primer: -40m3 fwd: Et from Amerisham  
High quality sequence stop: 1.  
Location/Qualifiers  
1..34 on/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:140910"  
/clone.lib="Soares\_cstis\_MHT"  
/sex="male"  
/lab\_host="DH10B"  
/note="Vector: pT730-pac (Pharmacia) with a modified  
polylinker. Site\_1: Not 1; Site\_2: Eco RI; 1st strand cDNA

BASE COUNT 15 a 10 c 15 g 10 t  
ORIGIN

Query Match 12.2% Score 14.6; DB 17; Length 50;  
Best Local Similarity 59.0%; Pred. No. 1.2e-06;  
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 8 CATAGTCACCTCTCAACCCACACCTCAT 36  
Db 34 CATAGTCGCTGCTAGCCCTCACTTAT 6

RESULT 91  
AA868967/c 34 bp mRNA linear EST 04-JAN-1999  
LOCUS  
DEFINITION  
3' similar to SM7524\_MOUSE P5395 PROTEIN TSG24. mRNA sequence.

ACCESSION  
AA868967  
VERSION  
EST.

KEYWORDS  
SOURCE  
human.

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps@mail.nih.gov  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.htm

was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGACCGCCCAATTTTITTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 9 a 9 c 9 g 7 t  
ORIGIN  
Query Match 12.0% Score 14.4; DB 9; Length 34;  
Best Local Similarity 65.6% Pred. No. 1.2e+06;  
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
OY 74 CCGTAAGATGATGCTTCCATAGCTGC 105  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 34 CCGTAAGATGCTTCCATAGCTGC 3

RESULT 92  
AA869987/c  
LOCUS  
DEFINITION  
vql0c01.r1 Barstead stromal cell line MFLR8B Mus musculus cDNA  
clone IMAGE:1093824 5' similar to SW:COX3\_RAT P05505 CYTOCHROME C  
OXIDASE POLYPEPTIDE III ; mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AA869987  
AA869987.1 GI:2965432  
EST.  
Mus musculus  
house mouse.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 34)  
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Maria M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:600056  
Trace considered overall poor quality  
Putative full length read  
Vector to vector length is 1058  
Possible reversed clone: similarity on wrong strand  
Seq primer: -28ml3 rev2 ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1..34  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1093824"  
/clone\_lib="Barstead stromal cell line MFLR8B"  
/cell\_line="C2C12 (undifferentiated)"  
/lab\_host="DH10B"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: EcoRI; Site\_2: NotI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5',  
TGTTACCAATCTGAAGTGGACCGCCCAATTTTITTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors  
[AATTCGATCTTC], digested with Not I and cloned into the  
Not I and Eco RI sites of the modified pT73 vector.  
Source undifferentiated tissue culture cell line C2C12.

TITLE  
JOURNAL  
COMMENT

FEATURES  
source  
1..34  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1608483"  
/clone\_lib="NCI-CCAP\_Kid5"  
/tissue\_type="2 pooled tumors (clear cell type)"  
/lab\_host="DH10B"  
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5',  
AACTGGGAAGATTCGGCCCAATTTTITTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M. Fatima Bonaldo.

library constructed by Bob Barstead. The C2C12 cell line  
(available from ATCC, catalog # CRL-1772) differentiates  
rapidly, forming contractile myotubes and producing  
characteristic muscle proteins.

BASE COUNT 9 a 8 g 10 t  
ORIGIN  
Query Match 12.0% Score 14.4; DB 9; Length 34;  
Best Local Similarity 75.0% Pred. No. 1.2e+06;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 92 GCTTCCATAGCTGCTGAATGTCAG 115  
||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 33 GCGTACATACCATCTGAATGTCAG 10

RESULT 93  
AA996016  
LOCUS  
DEFINITION  
OS26d10.s1 NCI-CCAP\_Kid5 Homo sapiens cDNA clone IMAGE:1608483 3'  
similar to TR:Q69340 Q69340 ORF1, ORF2, AND ORF3. ; contains MSRI.b1  
MSRI repetitive element ; mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AA996016  
AA996016.1 GI:3182505  
EST.  
human.  
Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 34)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 1092 Std Error: 0.00  
Seq primer: -40ml3 fwd ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1..34  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1608483"  
/clone\_lib="NCI-CCAP\_Kid5"  
/tissue\_type="2 pooled tumors (clear cell type)"  
/lab\_host="DH10B"  
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5',  
AACTGGGAAGATTCGGCCCAATTTTITTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 4 a 16 c 14 g 0 t  
ORIGIN  
Query Match 12.0% Score 14.4; DB 9; Length 34;  
Best Local Similarity 75.0% Pred. No. 1.2e+06;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 40 CCCCCCTCCAGAGGATTCAGGG 63  
 Db 5 CCCCCCTCCAGAGGAGGAGCCGGGG 28

RESULT 94  
 A2424085  
 LOCUS 38 bp DNA linear GSS 03-OCT-2003  
 DEFINITION 1M0203805R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0203805 R, DNA sequence.  
 A2424085  
 VERSION  
 KEYWORDS  
 SOURCE GSS.  
 ORGANISM Mus musculus  
 house mouse  
 REFERENCE 1. (bases 1 to 38)  
 AUTHORS Dunn,D., Ayaga,A., Barber,M., Becorn,T., Duval,B., Hamill,C.,  
 Isanase,L., Longacre,E., Renaud,M., Reenen,E., Reegen,T., Reilly,  
 M., Rose,M., Scott,R., Stokes,R., Thigley,A., von Niederhausern,A.,  
 and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT  
 84112, USA  
 Fax: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunngene@utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0203 row: B column: 05  
 Seq primer: CACAGGAGACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 38.  
 Location/Qualifiers  
 1..38  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0203805"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD29v. Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 ligated DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD2 (G114732114) (pAF129072.1), a copy-number  
 inducible derivative of plasmid p1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 1 a 30 c 0 g 7 t  
 ORIGIN  
 Query Match 12.0% Score 14.4; DB 17; Length 38;  
 Best Local Similarity 65.6% Pred No. 1.2e+06;  
 Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 17 CCCCCCTCCAGAGGATTCAGGG 48  
 Db 1 CCCCCCTCCAGAGGAGGAGCCGGGG 32

RESULT 95  
 A2591808  
 LOCUS 39 bp DNA linear GSS 27-APR-2001  
 DEFINITION 2M0276P1F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 clone UUGC2M0276P1 F, DNA sequence.  
 A2591808  
 VERSION  
 KEYWORDS  
 SOURCE GSS.  
 ORGANISM Mus musculus  
 house mouse  
 REFERENCE 1. (bases 1 to 39)  
 AUTHORS Dunn,D., Ayaga,A., Barber,M., Becorn,T., Duval,B., Hamill,C.,  
 Isanase,L., Longacre,E., Renaud,M., Reenen,E., Reegen,T., Reilly,  
 M., Rose,M., Scott,R., Stokes,R., Thigley,A., von Niederhausern,A.,  
 and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT  
 84112, USA  
 Fax: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunngene@utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0276 row: P column: 11  
 Seq primer: CGTTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 39.  
 Location/Qualifiers  
 1..39  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0276P1F"  
 /clone\_1lb="Mouse 10kb plasmid UUGC2M library"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD29v. Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 ligated DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD2 (G114732114) (pAF129072.1), a copy-number  
 inducible derivative of plasmid p1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

BASE COUNT 9 a 30 c 0 g 5 t  
 ORIGIN  
 Query Match 12.0% Score 14.4; DB 17; Length 39;  
 Best Local Similarity 65.5% Pred No. 1.1e+06;  
 Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 87 GATTGCTTCCATAGCTGCTGAATTCACCTTT 118  
 | | | | | | | | | | | | | | | | | | | |  
 Db 6 GGTGGATTCCTACTACTACTACTATTCACCTT 37  
 | | | | | | | | | | | | | | | | | | | |

RESULT 96  
 AA973240/c  
 LOCUS  
 DEFINITION 40 bp mRNA linear EST 27-AUG-1998  
 OT30805.s1 NCI-CGAP.GC3 Homo sapiens cDNA clone IMAGE:1597401 3'  
 similar to TR:015054 015054 KIA00346 ;, mRNA sequence.

ACCESSION  
 AA973240  
 VERSION  
 AA973240.1 GI:3148420  
 EST.  
 SOURCE  
 human.

ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 40)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
 JOURNAL  
 Tumor Gene Index  
 Unpublished (1997)  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution. Information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
 Insert Length: 420 Std Error: 0.00  
 Seq primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1. 40  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="NCI-CGAP.GC3"  
 /tissue\_type="pooled germ cell tumors"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; 1st strand cDNA was prepared from 3 pooled  
 germ cell tumors, and was then primed with a Not I -  
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
 RI adaptors (Pharmacia), digested with Not I and cloned  
 into the Not I and Eco RI sites of the modified pT73  
 vector. Library is not normalized. Library was  
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 3 a 15 c 21 g 1 t  
 ORIGIN

Query Match 12.0% Score 14.4; DB 9; Length 40;  
 Best Local Similarity 75.0%; Pred. NO. 1.3e+06;  
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 40 CCCACTCCAGAGGATTCAGGGG 63  
 | | | | | | | | | | | | | | | | | | | |  
 Db 35 CCCCCCCCCAGGGGGCTCTGGGG 12  
 | | | | | | | | | | | | | | | | | | | |

RESULT 97  
 BH797868  
 LOCUS  
 DEFINITION 40 bp DNA linear GSS 25-APR-2002  
 1008096A06.1EL\_x1 1008 - RescueMu Grid I Zea mays genomic, DNA  
 sequence.  
 ACCESSION  
 BH797868  
 VERSION  
 BH797868.1 GI:20307296  
 KEYWORDS  
 GSS.

SOURCE Zea mays.  
 ORGANISM  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 40)  
 Walbot.V.  
 Zea genomic sequences found using engineered RescueMu transposon  
 Unpublished (2001)  
 COMMENT  
 Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: [walbot@stanford.edu](mailto:walbot@stanford.edu)  
 Very probable ligation site of ends cut by single endonuclease.  
 Reverse complemented post-ligation sequence from source sequence.  
 Plate: 1008096 row: 26  
 Class: transposon-tagged.  
 Location/Qualifiers  
 1. 40  
 /organism="Zea mays"  
 /cultivar="mixed background W23/A188/B73"  
 /db\_xref="taxon:4577"  
 /clone\_lib="1008 - RescueMu Grid I"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Organ: leaf; Vector: RescueMu (engineered from  
 pBluescript backbone); Site: 1: BamHI. Site 2: BglII;  
 RescueMu is a 4.9 kb, modified maize Mu transposon  
 designed to allow plasmid rescue from total genomic DNA.  
 Mu elements insert preferentially into transcription  
 units. For more information on RescueMu, go to the web  
 site [www.zmndb.iastate.edu](http://www.zmndb.iastate.edu) and follow the links for  
 'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was  
 extracted from leaf punches, double digested using BamHI  
 and BglII, and ligated to form circular plasmids. DH10B  
 cells were transformed and then screened on LB plates with  
 ampicillin."

BASE COUNT 2 a 19 c 12 g 7 t  
 ORIGIN

Query Match 12.0% Score 14.4; DB 17; Length 40;  
 Best Local Similarity 75.0%; Pred. NO. 1.3e+06;  
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 53 GGATTCAGGGGTTCCAGCGTTCCT 76  
 | | | | | | | | | | | | | | | | | | | |  
 Db 5 GGCTCCAGGGGTTCCAGCGGTTTCCT 28  
 | | | | | | | | | | | | | | | | | | | |

RESULT 98  
 AA243755  
 LOCUS  
 DEFINITION 41 bp DNA linear GSS 03-OCT-2000  
 1M0203C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0203C23 F, DNA sequence.  
 ACCESSION  
 AA243755  
 VERSION  
 AA243755.1 GI:10547768  
 KEYWORDS  
 GSS.  
 SOURCE  
 house mouse.  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 41)  
 Dunn.D., Aoyagi.A., Barber.M., Beacorn.T., Duval.B., Hamil.C.,  
 Islam.H., Longacre.S., Mahmoud.M., Meenen.E., Pedersen.T., Reilly  
 M., Rose.M., Rose.R., Stokes.R., Tingey.A., von Niederhausern,A.  
 and Wright.D. Weiss.R.  
 TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL  
 Unpublished (2000)



```

/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen INTS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5'-
AAGCGAAGATTAAATTAAGATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Falima Ronaldo."

```

```

BASE COUNT      11 a      8 c      11 g      11 t      2 others
ORIGIN
Query Match      12.0%; Score 14.4; DB 9; Length 43;
Best Local Similarity 69.2%; Pred No. 1.3e+06;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY      71 GTTCCTGAAATGATCGATGGCTTC 96
      | | | | | | | | | | | | | |
DB      31 GATANGACAATGATCGATATCCTTC 6

```

```

Search completed: June 17, 2003, 22:01:41
Job time : 1381 secs

```